

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 11:04:30 ; Search time 13.05 Seconds
(without alignments)
591.455 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 316
Sequence: 1 MRRASRDYKYLRSSEMG.....LLDPDQATYFGAFKVDID 316

Scoring table: OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

d size : 0
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	316	100.0	316	2	US-08-842-842-7
2	316	100.0	316	4	US-08-989-362-2
3	316	100.0	316	4	US-09-052-521C-2
4	217	68.7	294	3	US-08-996-139-11
5	217	68.7	294	4	US-08-995-659-11
6	217	68.7	294	4	US-09-215-649A-11
7	27	8.5	28	4	US-09-052-521C-34
8	22	7.0	27	4	US-09-052-521C-33
9	22	7.0	317	3	US-08-996-139-13
10	22	7.0	317	4	US-08-995-659-13
11	22	7.0	317	4	US-09-215-649A-13
12	22	7.0	317	4	US-09-052-521C-4
13	17	5.4	17	4	US-09-052-521C-35
14	8	2.5	459	2	US-08-870-518-2
15	8	2.5	4472	2	US-08-804-227C-2
16	7	2.2	21	2	US-08-997-080-4
17	7	2.2	21	2	US-08-997-352-4
18	7	2.2	21	3	US-08-873-970-4
19	7	2.2	21	4	US-09-095-855-4
20	7	2.2	21	4	US-08-705-347A-4
21	7	2.2	21	4	US-09-324-542-4
22	7	2.2	21	2	US-08-640-847C-3
23	7	2.2	41	2	US-08-640-847C-9
24	7	2.2	41	2	US-08-640-847C-12
25	7	2.2	58	2	US-08-284-391B-35
26	7	2.2	58	4	US-09-218-950-35
27	7	2.2	93	1	US-08-591-498-10

28	7	2.2	93	1	US-08-591-498-14	Sequence 14, Appl
29	7	2.2	117	3	US-08-702-609A-4	Sequence 4, Appl
30	7	2.2	117	3	US-08-702-609A-6	Sequence 6, Appl
31	7	2.2	190	3	US-08-799-149C-3	Sequence 3, Appl
32	7	2.2	207	4	US-09-199-637A-211	Sequence 211, App
33	7	2.2	223	4	US-09-171-461-11	Sequence 11, Appl
34	7	2.2	301	1	US-08-420-235B-47	Sequence 47, Appl
35	7	2.2	301	2	US-08-343-101A-22	Sequence 22, Appl
36	7	2.2	301	3	US-09-183-688-22	Sequence 22, Appl
37	7	2.2	301	4	US-08-793-624-47	Sequence 47, Appl
38	7	2.2	337	2	US-08-861-464-12	Sequence 12, Appl
39	7	2.2	337	2	US-08-396-001-12	Sequence 12, Appl
40	7	2.2	337	4	US-09-323-433A-12	Sequence 12, Appl
41	7	2.2	370	4	US-09-142-551A-4	Sequence 4, Appl
42	7	2.2	375	3	US-08-872-979-3	Sequence 3, Appl
43	7	2.2	396	4	US-09-142-551A-3	Sequence 3, Appl
44	7	2.2	422	2	US-08-485-938A-34	Sequence 34, Appl
45	7	2.2	468	2	US-08-390-000A-7	Sequence 7, Appl
46	7	2.2	472	1	US-08-194-338-6	Sequence 6, Appl
47	7	2.2	477	1	US-08-444-734A-4	Sequence 4, Appl
48	7	2.2	477	1	US-08-087-772A-16	Sequence 16, Appl
49	7	2.2	660	3	US-09-111-085-2	Sequence 2, Appl
50	7	2.2	660	4	US-09-376-781-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-842-7

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYKYLRSSEMGSGPGVHEGPHLPAPAPAPAPPAAASRMFLALGLGLGQ 60
DB 1 MRRASRDYKYLRSSEMGSGPGVHEGPHLPAPAPAPAPPAAASRMFLALGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESEDLPDSCRMKQ 120

Db 61 VVCSIALFLYFRAQMDPNRISESDTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120
QY 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAAISIPSGSHK 180
Db 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAAISIPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLVMY 240
Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLVMY 240
QY 241 VVKTISKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLAGEEISIQVSNPSLLDP 300
Db 241 VVKTISKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316

ILT 2

08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Mattson, Jeanine D.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; TITLE OF INVENTION: Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-362-2

Query Match 100.0%; Score 316; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKLYRSSEMGSGPGVHEGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYGYKLYRSSEMGSGPGVHEGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60

QY 61 VVCSIALFLYFRAQMDPNRISESDTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120
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QY 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAAISIPSGSHK 180
Db 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAAISIPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLVMY 240
Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLVMY 240
QY 241 VVKTISKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLAGEEISIQVSNPSLLDP 300
Db 241 VVKTISKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316

RESULT 3

US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mouse
US-09-052-521C-2

Query Match 100.0%; Score 316; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYGYKLYRSSEMGSGPGVHEGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYGYKLYRSSEMGSGPGVHEGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISESDTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISESDTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120
QY 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAAISIPSGSHK 180
Db 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAAISIPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLVMY 240
Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLVMY 240
QY 241 VVKTISKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLAGEEISIQVSNPSLLDP 300
Db 241 VVKTISKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316

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RESULT      4
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
08-996-139-11

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	Query Match	68.7%	Score 217;	DB 3;	Length 294;	
	Best Local Similarity	100.0%;	Pred. No. 6.7e-210;			
	Matches 217; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
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Db	78 LQDSTFLESEDTLPDSICRRMKAFQAGVQKELOHIVGPORFSGAPAMMEGSLMDVAQRGKP	137				
QY	160 EAQFPAHLTINAAIPSGSHKVTLSWYHDRGWAKISNMTLSNGKLRYNQDGFFYYLYANI	219				
Db	138 EAQFPAHLTINAAIPSGSHKVTLSWYHDRGWAKISNMTLSNGKLRYNQDGFFYYLYANI	197				
QY	220 CFRHHETSGSVPTDYQLQMWTVVKTSTIKIPSSHNLMKGSTKNNSGNSEFHFYFSINVGGF	279				
Db	198 CFRHHETSGSVPTDYQLQMWTVVKTSTIKIPSSHNLMKGSTKNNSGNSEFHFYFSINVGGF	257				
QY	280 FKLARGEIISTQVSNPSSLDDPDQDATYFGAFKVQDID	316				
Db	258 FKLARGEIISTQVSNPSSLDDPDQDATYFGAFKVQDID	294				

RESULT 5

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US-08-659-11
: Sequence 11, Application US/08995659
: Patent No. 624213
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/995,659
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION NUMBER:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-995-659-11

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[illegible]

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RESULT      6
US-09-215-649A-11
; Sequence 11, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; .. APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; 9-215-649A-11
Query Match          68.7%; Score 217; DB 4; Length 294;
Best Local Similarity 100.0%; Pred.No. 6.7e-210;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LQSTLSEDTLPDSCRRMKQAFQGVKQLQHIVGQRFSGAPAMEGSWLDVAQRGKP 159
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Db 78 LQSTLSEDTLPDSCRRMKQAFQGVKQLQHIVGQRFSGAPAMEGSWLDVAQRGKP 137
|||||
QY 160 EAQPFALHTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRYNDQGFYYLYANI 219
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Db 138 EAQPFALHTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRYNDQGFYYLYANI 197
|||||
QY 220 CFRHHETSGSVPTDYLLQLVVYVKVTISKIPSSHNLKMGSTKNNSGNSEHFYSINVGGF 279
|||||
Db 198 CFRHHETSGSVPTDYLLQLVVYVKVTISKIPSSHNLKMGSTKNNSGNSEHFYSINVGGF 257
|||||
QY 280 FKLRAGEEISTQVSNPILLSDDPDQDATYFGAFKVQDID 316
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Db 258 FKLRAGEEISTQVSNPILLSDDPDQDATYFGAFKVQDID 294
|||||

```

;; GENERAL INFORMATION:
;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/996,139
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;;
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/996,139
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;;
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; CLASSIFICATION:
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 317 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-996-139-13

Query Match 7.0%; Score 22; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VNQDGFYLYANICFRHHETSG 228
Db 208 VNQDGFYLYANICFRHHETSG 229

RESULT 10
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/995,659
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;;
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; CLASSIFICATION:
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 317 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-995-659-13

Query Match 7.0%; Score 22; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VNQDGFYLYANICFRHHETSG 228
Db 208 VNQDGFYLYANICFRHHETSG 229

RESULT 11
US-09-215-649A-13
; Sequence 13, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
99-215-649A-13

Query Match 7.0%; Score 22; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VNQDGFYLYANICFRHHETSG 228
|||||
Db 208 VNQDGFYLYANICFRHHETSG 229

RESULT 12
US-09-052-521C-4
; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4

Query Match 7.0%; Score 22; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VNQDGFYLYANICFRHHETSG 228
|||||
Db 208 VNQDGFYLYANICFRHHETSG 229

RESULT 13
US-09-052-521C-35
; Sequence 35, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C

; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-052-521C-35

Query Match 5.4%; Score 17; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 VYVVKTSIKIPSSHNL 255
|||||
Db 1 VYVVKTSIKIPSSHNL 17

RESULT 14
US-08-870-518-2
; Sequence 2, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Galcheva-Gargova, Zoya
; TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,518
; FILING DATE: 06-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,219
; FILING DATE: 06-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/102001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-870-518-2

Query Match 2.5%; Score 8; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPPA 44
|||||
Db 20 PAPAPPPA 27

RESULT 15

US-08-804-227C-2
; Sequence 2, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rostock, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4472 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-804-227C-2

Query Match 2.5%; Score 8; DB 2; Length 4472;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 PSAPAPAP 41
|||||
Db 4442 PSAPAPAP 4449

RESULT 16

US-08-997-080-4
; Sequence 4, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-080-4

Query Match 2.2%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPP 43
|||||
Db 2 PAPAPPP 8

RESULT 17

US-08-997-362-4
; Sequence 4, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997

; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-997-362-4

Query Match 2.2%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPP 43
Db 2 PAPAPPP 8

RESULT 18
US-08-873-970-4
; Sequence 4, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-995-855-4

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-873-970-4

Query Match 2.2%; Score 7; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPP 43
Db 2 PAPAPPP 8

RESULT 19
US-09-095-855-4
; Sequence 4, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-095-855-4

Query Match 2.2%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPP 43
Db 2 PAPAPPP 8

RESULT 20

US-08-705-347A-4

; Sequence 4, Application US/08705347A
; Patent No. 6284255
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,347A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206.269.0565
; TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 2.2%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPP 43
Db 2 PAPAPPP 8

RESULT 21

US-09-324-542-4

; Sequence 4, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324, 542
; CURRENT FILING DATE: 1999-06-02

Query Match 2.2%; Score 7; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 7.1;

; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-4

Query Match 2.2%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 PAPAPPP 43

Db 2 PAPAPPP 8

RESULT 22

US-08-640-847C-3

; Sequence 3, Application US/08640847C
; Patent No. 5993865
; GENERAL INFORMATION:
; APPLICANT: BECH, Lene M.
; APPLICANT: SORENSEN, Steen B.
; APPLICANT: VAAG, Pia
; APPLICANT: MULDEJERG, Marianne
; APPLICANT: BEENFELDT, Thorild
; APPLICANT: LEAH, Robert
; APPLICANT: BREDDAM, Klaus
; TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; ZIP: 10023
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44 MB
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: Wordperfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,847C
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 426

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK94/00420
; FILING DATE: 08-NOV-1994
; APPLICATION NUMBER: DK001266/93
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010781-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1890
; TELEFAX: (212) 246-8959
; TELEX: 233288

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 Amino Acids
; TYPE: Amino Acids
; TOPOLOGY: Linear

US-08-640-847C-3

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NAAIPS 176
|||||||
Db 15 NAAIPS 21

RESULT 23

US-08-640-847C-9
; Sequence 9, Application US/08640847C
; Patent No. 5993865

GENERAL INFORMATION:

APPLICANT: BECH, Lene M.
APPLICANT: SORESEN, Steen B.
APPLICANT: VAAG, Pia
APPLICANT: MULDBJERG, Marianne
APPLICANT: BEENFELDT, Thorild
APPLICANT: LEAH, Robert
APPLICANT: BREDDAM, Klaus

TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
ZIP: 10023

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/4" Disk 1.44 MB
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

SOFTWARE: WordPerfect 8 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/640.847C

FILING DATE: 26-JUN-1996

CLASSIFICATION: 426

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK94/00420

FILING DATE: 08-NOV-1994

APPLICATION NUMBER: DK001266/93

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: MASS, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-010781-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1890

TELEFAX: (212) 246-8959

TELEX: 233288

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 Amino Acids

TYPE: Amino Acids

TOPOLOGY: Linear

US-08-640-847C-9

Query Match 2.2%; Score 7; DB 2; Length 41;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NAAIPS 176
|||||||
Db 15 NAAIPS 21

RESULT 24

US-08-640-847C-12
; Sequence 12, Application US/08640847C
; Patent No. 5993865

GENERAL INFORMATION:

APPLICANT: BECH, Lene M.

APPLICANT: SORESEN, Steen B.

APPLICANT: VAAG, Pia

APPLICANT: MULDBJERG, Marianne

APPLICANT: BEENFELDT, Thorild

APPLICANT: LEAH, Robert

APPLICANT: BREDDAM, Klaus

APPLICANT: SORESEN, Steen B.
APPLICANT: VAAG, Pia
APPLICANT: MULDBJERG, Marianne
APPLICANT: BEENFELDT, Thorild
APPLICANT: LEAH, Robert
APPLICANT: BREDDAM, Klaus
TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: LADAS & PARRY

STREET: 26 WEST 61 STREET

CITY: NEW YORK

STATE: NY

ZIP: 10023

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/4" Disk 1.44 MB

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

SOFTWARE: WordPerfect 8 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/640.847C

FILING DATE: 26-JUN-1996

CLASSIFICATION: 426

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK94/00420

FILING DATE: 08-NOV-1994

APPLICATION NUMBER: DK001266/93

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: MASS, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-010781-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1890

TELEFAX: (212) 246-8959

TELEX: 233288

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 Amino Acids

TYPE: Amino Acids

TOPOLOGY: Linear

US-08-640-847C-12

Query Match

Best Local Similarity 100.0%; DB 2; Length 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NAAIPS 176
|||||||
Db 15 NAAIPS 21

RESULT 25

US-08-284-391B-35

; Sequence 35, Application US/08284391B

; Patent No. 5851828

; GENERAL INFORMATION:

APPLICANT: Seed, Brian

APPLICANT: Banapour, Babak

APPLICANT: Romeo, Charles

APPLICANT: Kolanus, Waldemar

TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

US-08-284-391B-35

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-391B-35

Query Match 2.2%; Score 7; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LLGLGLG 59
Db 43 LLGLGLG 49

RESULT 26
US-09-218-950-35
Sequence 35, Application US/09218950
Patent No. 6284240
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391

FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-218-950-35

Query Match 2.2%; Score 7; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LLGLGLG 59
Db 43 LLGLGLG 49

RESULT 27
US-08-591-498-10
Sequence 10, Application US/08591498
Patent No. 5773694
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
PILLSBURY MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,498
FILING DATE: 25-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01636
FILING DATE: 29-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317816.8
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9316158.6
FILING DATE: 04-AUG-1993
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: PAPI
US-08-591-498-10

Query Match 2.2%; Score 7; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NAASIPS 176
Db 67 NAASIPS 73

RESULT 28
US-591-498-14
Sequence 14, Application US/08591498
Patent No. 5773694
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,498
FILING DATE: 25-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01636
FILING DATE: 29-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317816.8
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9316158.6
FILING DATE: 04-AUG-1993
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Zm-nsLTP
US-08-591-498-14

Query Match 2.2%; Score 7; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NAASIPS 176

Db 67 NAASIPS 73

RESULT 29

US-08-702-609A-4
Sequence 4, Application US/08702609A
Patent No. 6031152
GENERAL INFORMATION:
APPLICANT: Olsen, Odd-Arne
APPLICANT: Kalla, Roger
APPLICANT: Linnestad, Casper
TITLE OF INVENTION: Promoter from a Lipid
TITLE OF INVENTION: Transfer Protein Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Plant Molecular Biology Laboratory,
ADDRESSEE: Department of Biotechnical Sciences, Agricultural
ADDRESSEE: University of No. 6031152way and Agricultural Biotechnology
ADDRESSEE: Program NRC
COUNTRY: No. 6031152way
ZIP: N-1432
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 98
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,609A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NO95/00042
FILING DATE: 23.02.95
ATTORNEY/AGENT INFORMATION:
NAME: Thaddius J. Carvis
REGISTRATION NUMBER: 26110
REFERENCE/DOCKET NUMBER: 833-P0016A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 residues
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Barley
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Linnestad, Casper
AUTHORS: Lonneborg, Anders
AUTHORS: Kalla, Roger
AUTHORS: Olsen, Odd-Arne
TITLE: Promoter of a Lipid Transfer Protein Gene
TITLE: Expressed in Barley Aleurone Cells Contains
TITLE: Similar myb and myc Recognition Sites as the Maize
TITLE: Bz-McC Allele
JOURNAL: Plant Physiol.
VOLUME: 97
PAGES: 842
DATE: 17.06.91
US-08-702-609A-4

Query Match 2.2%; Score 7; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NAASIPS 176

Db 91 NNASIPS 97

RESULT 30

US-08-702-609A-6

; Sequence 6, Application US/08702609A

; Patent No. 6031152

; GENERAL INFORMATION:

; APPLICANT: Olsen, Odd-Arne

; APPLICANT: Kalla, Roger

; APPLICANT: Linnestad, Casper

; TITLE OF INVENTION: Promoter from a Lipid

; TITLE OF INVENTION: Transfer Protein Gene

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Plant Molecular Biology Laboratory,

; ADDRESSEE: Department of Biotechnical Sciences, Agricultural

; ADDRESSEE: University of No. 6031152way and Agricultural Biotechnology

; ADDRESSEE: Program NRC

; COUNTRY: No. 6031152way

; ZIP: N-1432

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" 1.44 Mb diskette

; COMPUTER: IBM PC

; OPERATING SYSTEM: WINDOWS 98

; SOFTWARE: Word Processing

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08702,609A

; FILING DATE: 20-NOV-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/NO95\00042

; FILING DATE: 23.02.95

; ATTORNEY/AGENT INFORMATION:

; NAME: Thaddius J. Carvils

; REGISTRATION NUMBER: 26110

; REFERENCE/DOCKET NUMBER: 833-P0016A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 203-324-6155

; TELEFAX: 203-327-1096

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 residues

; TYPE: amino acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE:

; ORIGINAL SOURCE:

; ORGANISM: Barley

; PUBLICATION INFORMATION:

; AUTHORS:

; AUTHORS: Skriver, Karen

; AUTHORS: Leah, Robert

; AUTHORS: Muller-Urli, Frieder

; AUTHORS: Olsen, Finn-Lok

; AUTHORS: Mundy, John

; TITLE: Structure and Expression of the Barley Lipid Transfer Protein Promoter of

; JOURNAL: Plant Molecular Biology

; VOLUME: 18

; PAGES: 587

; DATE: 16.09.91

US-08-702-609A-6

Query Match 2.2%; Score 7; DB 3; Length 117;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 NNASIPS 176

; | | | | |

Db 91 NNASIPS 97

RESULT 31

US-08-799-149C-3

; Sequence 3, Application US/08799149C

; Patent No. 6008195

; GENERAL INFORMATION:

; APPLICANT: Michael E. Selsted

; TITLE OF INVENTION: Antimicrobial Peptides and

; TITLE OF INVENTION: Methods of Use

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08799,149C

; FILING DATE: 14-February-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/011,834

; FILING DATE: 16-February-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Lisa A. Halle, Ph.D.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07306/009001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 190 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Coding sequence

; LOCATION: 39..598

US-08-799-149C-3

Query Match 2.2%; Score 7; DB 3; Length 190;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 LALLGLG 57

; | | | | |

Db 13 LALLGLG 19

RESULT 32

US-09-199-637A-211

; Sequence 211, Application US/09199637A

; Patent No. 6355411

; GENERAL INFORMATION:

; APPLICANT: Ausubel, Frederick

; APPLICANT: Goodman, Howard M.

; APPLICANT: Rahme, Laurence G.

; APPLICANT: Mahajan-Miklos, Shalina

; APPLICANT: Tan, Man-Wah

; APPLICANT: Cao, Hui

; APPLICANT: Drenkard, Eliana

; APPLICANT: Tsongalis, John

; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID

; TITLE OF INVENTION: SEQUENCES AND USES THEREOF

; FILE REFERENCE: 00786/361002

; CURRENT APPLICATION NUMBER: US/09/199,637A

; CURRENT FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-211

Query Match 2.2%; Score 7; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 APSAPAP 39
Db 89 APSAPAP 95

ULT 33
09-171-461-11
; Sequence 11, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:

; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chioccia, Susanna
; APPLICANT: Kurzbauer, Robert
; APPLICANT: Schaffner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171,461
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; EARLIER FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 223
; TYPE: PRT
; ORGANISM: CELO Virus
; FEATURE:
; OTHER INFORMATION: Position: 17559..18230 /gene: L3 /product: L3 pVI
US-09-171-461-11

Query Match 2.2%; Score 7; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 APAPAPP 42
Db 143 APAPAPP 149

RESULT 34
US-08-420-235B-47
; Sequence 47, Application US/08420235B
; Patent No. 5801042
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/420,235B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-420-235B-47

Query Match 2.2%; Score 7; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 GLGLGV 61
Db 42 GLGLGV 48

RESULT 35
US-08-343-101A-22
; Sequence 22, Application US/08343101A
; Patent No. 5830759
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
; TITLE OF INVENTION: Virus Sequences And Uses Thereof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,101A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-343-101A-22

Query Match 2.2%; Score 7; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GLGLGQV 61
|||
Db 42 GLGLGQV 48

Search completed: July 15, 2002, 11:06:45
Job time: 135 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 11:06:51 ; Search time 13.45 Seconds
(without alignments)
909.694 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 316
Sequence: 1 MRRASRDYKYLRSSEMG.....LLDPQDATYFGAFKVDID 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	316	100.0	316	1	TN11_MOUSE
2	22	7.0	317	1	TN11_HUMAN
3	9	2.8	473	1	BIAR_CANFA
4	9	2.8	633	1	PAN2_HUMAN
5	8	2.5	173	1	HES2_HUMAN
6	8	2.5	194	1	MLEV_HUMAN
7	8	2.5	206	1	GPBB_HUMAN
8	8	2.5	208	1	GPBB_PAPCY
9	8	2.5	398	1	B3AR_FELCA
10	8	2.5	459	1	ZPRI_HUMAN
11	8	2.5	1193	1	DP3A_XYLFA
12	8	2.5	1425	1	MADI_HUMAN
13	7	2.2	91	1	NULM_BRALA
14	7	2.2	96	1	NULM_PETMA
15	7	2.2	99	1	NLT4_ORYSA
16	7	2.2	116	1	NLT1_ORYSA
17	7	2.2	117	1	NLT1_HORVU
18	7	2.2	117	1	NLT3_ORYSA
19	7	2.2	118	1	NLT3_ORYSA
20	7	2.2	118	1	NLT2_ORYSA
21	7	2.2	120	1	NLTP_MAIZE
22	7	2.2	135	1	NIUL_RHOCA
23	7	2.2	198	1	PENT_HUMAN
24	7	2.2	209	1	HIA_XENLA
25	7	2.2	223	1	P1V6_ADEG1
26	7	2.2	240	1	CD7_HUMAN
27	7	2.2	243	1	TRIC_XENLA
28	7	2.2	251	1	HXB4_HUMAN
29	7	2.2	267	1	LYL1_HUMAN
30	7	2.2	268	1	CDX1_MOUSE
31	7	2.2	272	1	TNR4_MOUSE
32	7	2.2	301	1	VP23_EBV
33	7	2.2	309	1	HXB1_CHICK

34	7	2.2	313	1	GAG_AVISN	P03342 avian splce
35	7	2.2	337	1	NCA3_YEAST	P46955 saccharomyc
36	7	2.2	342	1	PYRC_SYNY3	P74438 synchococyt
37	7	2.2	344	1	COMC_METJA	Q58820 methanococ
38	7	2.2	348	1	CEBB_BOVIN	O02755 bos taurus
39	7	2.2	354	1	PROW_SALTY	P17327 salmonella
40	7	2.2	391	1	HERP_HUMAN	Q15011 homo sapien
41	7	2.2	400	1	MKK2_HUMAN	P49137 homo sapien
42	7	2.2	402	1	ODP2_MYCPN	P75392 mycoplasma
43	7	2.2	405	1	B3AR_CANFA	O02662 canis fami
44	7	2.2	407	1	G110_HUMAN	Q16186 homo sapien
45	7	2.2	407	1	G110_MOUSE	Q9Jkv1 mus musculu
46	7	2.2	407	1	G110_RAT	Q9Jmb5 rattus norv
47	7	2.2	408	1	BTNI_YEAST	P47040 saccharomyc
48	7	2.2	422	1	PAFA_CHICK	Q90678 g platelet-
49	7	2.2	426	1	ASD4_NEUCR	Q9hev5 neurospora
50	7	2.2	446	1	KLF5_MOUSE	Q920z7 mus musculu

ALIGNMENTS

RESULT 1

ID	TN11_MOUSE	STANDARD;	PRT;	316 AA.
AC	O35235; O35306;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (OPF) (Osteoclastogenesis-inhibitory factor) (OCIF).			
DE	TNFSF11 OR RANKL OR TRANCE OR OPGL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hybridoma;			
RX	MEDLINE=97460112; PubMed=9312132;			
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlick J., Chao M.,			
RA	Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,			
RA	Choi Y.,			
RT	"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."			
RL	J. Biol. Chem. 272:25190-25194(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=98227661; PubMed=9568710;			
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,			
RA	Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,			
RA	Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,			
RA	Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,			
RA	Boyle W.J.;			
RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."			
RL	Cell 93:165-176(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow stroma;			
RX	MEDLINE=98188248; PubMed=9520411;			
RA	Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,			
RA	Mochizuki S.-I., Tomoyasu A., Yan K., Goto M., Murakami A., Tsuda E.,			
RA	Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;			
RT	"Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).			
RN	[4]			

RP SEQUENCE FROM N.A.
RC TISSUE=Thymic lymphoma;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ikeda T.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC TRABECULAR BONE AND LUNG.
CC DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBULO-
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS, WITH
CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC HYPERTROPHIC CHONDROCYTES.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL; AF053713; AAC40113.1; -
DR EMBL; AF013170; AAC71061.1; -
DR EMBL; AB08426; BAA35425.1; -
DR EMBL; AF019048; AAB86812.1; -
DR EMBL; AB036798; BAA37259.1; -
DR MGD; MGI:1100089; Tnfsf11.
DR InterPro; IPR003263; TNF.5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF.5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF.1; FALSE_NEG.
DR PROSITE; PS50049; TNF.2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 48
FT TRANSMEM 49 69
FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 70 316
FT CARBOHYD 197 197
FT CARBOHYD 262 262
FT CONFLICT 99 99
FT CONFLICT 99 99
SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE0967A CRC64;

Query Match 100.0%; Score 316; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKGLYRSSEMGSGPGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60
DB 1 MRRASRDYKGLYRSSEMGSGPGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLGQ 60

QY 61 VVCSIALFLYFRAQMDPNRISEDTHCFYRILRLHENAAGLDSTLESDTLPDSCRRMKQ 120
DB 61 VVCSIALFLYFRAQMDPNRISEDTHCFYRILRLHENAAGLDSTLESDTLPDSCRRMKQ 120
QY 121 AFGAVOKELQHVGPORFSGAPAMMEGSLDVAORCKPEAQPFAHLTINAAISIPSGSHK 180
DB 121 AFGAVOKELQHVGPORFSGAPAMMEGSLDVAORCKPEAQPFAHLTINAAISIPSGSHK 180
QY 181 VTLSWYHDSRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHTSGSVPTDYQLVMVY 240
DB 181 VTLSWYHDSRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHTSGSVPTDYQLVMVY 240
QY 241 VVTSIKIPSHNLKMGSTKNWSEFHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSHNLKMGSTKNWSEFHFYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DDATYFAGAFKVDID 316
DB 301 DDATYFAGAFKVDID 316
RESULT 2
TN11_HUMAN STANDARD; PRT; 317 AA.
AC Q14788; O14723; Q9P2Q3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
DE TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, and Peripheral blood;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RP SEQUENCE OF 73-317 FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Tongue;

RX MEDLINE-20175237; PubMed-10708588;
RA Nagai M., Kyakumoto S., Sato N.;
RT "Cancer cells responsible for humoral hypercalcemia express mRNA
RT encoding a secreted form of ODF/TRANCE that induces osteoclast
RL formation.";
RL Biochem Biophys. Res. Commun. 269:532-536(2000).
CC -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC HYPERCALCEMIA OF MALIGNANCY.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC SECRETED (ISOFORM 2).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2(SODF; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; AF019047; AAC86811.1; -;
DR EMBL; AF053712; AAC39731.1; -;
DR EMBL; AF013171; AAC51762.1; -;
DR EMBL; AB037599; BAA90488.1; -;
DR MIM; 602642; -;
DR InterPro: IPR003263; TNF-5.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF-5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF-1; FALSE_NEG.
DR PROSITE; PS50049; TNF-2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing.
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
DOMAIN 69 317 EXTRACELLULAR (POTENTIAL).
CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 73 MISSING (IN ISOFORM 2).
FT CONFLICT 194 194 A -> G (IN REF. 3).
SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 7.0%; Score 22; DB 1; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VNQDGFYLYANICFRHETSG 228
|||||
DB 208 VNQDGFYLYANICFRHETSG 229

RESULT 3
BIAR_CANFA STANDARD; PRT; 473 AA.
AC P79148;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Beta-1 adrenergic receptor.

GN ADRL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Flissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97364078; PubMed-9220370;
RA Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascieri M.A.,
RA Fong T.M.;
RT "Molecular cloning of the dog beta 1 and beta 2 adrenergic
RT receptors.";
RL J. Recept. Signal Transduct. Res. 17:599-607(1997).
CC -!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
CC APPROXIMATELY EQUAL AFFINITY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U73207; AAB93648.1; -;
DR HSSP; P07700; IDEP.
DR GCRdb; GCR_1183; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 80 83 1 (POTENTIAL).
FT DOMAIN 84 96 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 97 120 2 (POTENTIAL).
FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 155 3 (POTENTIAL).
FT DOMAIN 156 175 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 199 4 (POTENTIAL).
FT DOMAIN 200 221 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 222 245 5 (POTENTIAL).
FT DOMAIN 246 322 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 323 346 6 (POTENTIAL).
FT DOMAIN 347 353 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 354 377 7 (POTENTIAL).
FT DOMAIN 378 473 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (PROBABLE).
FT DISULFID 131 209 BY SIMILARITY.
FT MOD_RES 309 309 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT LIPID 389 389 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 473 AA; 50060 MW; 361357F7DF9DBD7E CRC64;

Query Match 2.8%; Score 9; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 APAPAPPPA 44
|||||
DB 278 APAPAPPPA 286

RESULT 4

PAN2_HUMAN STANDARD; PRT; 633 AA.
AC Q96RD6; Q96RD5; Q9UCX8;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Panexin 2.
GN PANX2.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Baranova A., Ivanov D., Skoblov M., Pestova A., Kelmanson I.,
RA Shagin D., Usman N., Lukyanov S., Panchin Y.;
RT "Mammalian pannexin family homologs to invertebrate gap-junction
RT proteins are differentially expressed in nervous tissue.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
PN [2]
SEQUENCE FROM N.A.
MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA Baguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA Burton J., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Cobley V., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Dockree C.,
RA Dodsworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M.,
RA Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E.,
RA Grahm D., Griffiths M.N., Hall C., Hall R., Hall-Tamlyn G.,
RA Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Leversha M.A.,
RA Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M.,
RA Matthews L., Mccann O.T., Mcclay J., McLaren S., Mccurray A.A.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Sulston J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M.,
RA Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
RA Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Mitsuyma S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E.,
RA Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Williamson D.,
RA Wu H., Yao Z., Zhan M., Zhang G., Chissos S., Murray J., Miller N.,
RA Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
RA Rohlfs J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P.,
RA Nelson J., Korf I., Bedell J.A., Hillier L.A., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE GAP JUNCTIONS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE INNEKIN FAMILY.
CC
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CC
CC EMBL; AL031848; CAB46198.1; -;
DR EMBL; AL031848; CAB46199.1; -;
DR InterPro: IPR003015; HLH_Myc.
DR InterPro: IPR001092; HLH_dim.
DR InterPro: IPR003650; Orange.
DR Pfam: PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.

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DR EMBL; AF398510; AAK91715.1; -;
DR EMBL; AF398511; AAK91716.1; -;
DR EMBL; AL023228; CAB63042.1; -;
KW Gap junction; Transmembrane; Alternative splicing.
FT TRANSMEM 38 60 POTENTIAL.
FT TRANSMEM 114 136 POTENTIAL.
FT TRANSMEM 217 239 POTENTIAL.
FT TRANSMEM 283 305 POTENTIAL.
FT VARSPPLIC 1 124 MISSING (IN ISOFORM 2).
SQ SEQUENCE 633 AA; 69478 MW; C89CF833E0251D58 CRC64;

Query Match 2.8%; Score 9; DB 1; Length 633;
Best Local Similarity 100.0%; Pred. No. 0.45; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 36 APAPAPPPA 44
| | | | | | | | | |
Db 486 APAPAPPPA 494

RESULT 5
ID HES2_HUMAN STANDARD; PRT; 173 AA.
AC Q9Y543; Q9Y542;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor HES-2 (Hairy and enhancer of split 2).
GN HES2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Howden P.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
CC PROTEIN FOR THEIR TRANSCRIPTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
CC RATHER THAN THE CANONICAL E-BOX (CANNTG).
CC -!- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL
CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
CC HAIRY-RELATED PROTEINS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
CC
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CC
CC EMBL; AL031848; CAB46198.1; -;
DR EMBL; AL031848; CAB46199.1; -;
DR InterPro: IPR003015; HLH_Myc.
DR InterPro: IPR001092; HLH_dim.
DR InterPro: IPR003650; Orange.
DR Pfam: PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.

GenCore version 4.5
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OM.protein - protein search, using sw model

Run on: July 15, 2002, 11:01:05 ; Search time 13.12 Seconds
(without alignments)
588.299 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 1675
Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPDQDATYFGAFKVVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

al number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCrUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	2	US-08-842-842-7
2	1675	100.0	316	4	US-08-989-362-2
3	1675	100.0	316	4	US-09-052-521C-2
4	1554	92.8	294	3	US-08-996-139-11
5	1554	92.8	294	4	US-08-995-659-11
6	1554	92.8	294	4	US-09-215-649A-11
7	1417.5	84.6	317	3	US-08-996-139-13
8	1417.5	84.6	317	4	US-08-995-659-13
9	1417.5	84.6	317	4	US-09-215-649A-13
10	1417.5	84.6	317	4	US-09-052-521C-4
11	258.5	15.4	279	4	US-09-072-993C-3
12	258.5	15.4	281	1	US-08-670-354-2
13	258.5	15.4	281	3	US-08-584-031-1
14	258.5	15.4	281	3	US-08-780-496-1
15	258.5	15.4	281	4	US-08-883-086-10
16	258.5	15.4	281	4	US-09-320-424-2
17	258.5	15.4	281	4	US-09-333-593A-6
18	258.5	15.4	281	5	PCT-US96-10895-2
19	244	14.6	291	1	US-08-670-354-6
20	244	14.6	291	4	US-09-320-424-6
21	244	14.6	291	5	PCT-US96-10895-6
22	244	14.3	256	4	US-09-320-424-13
23	236	14.1	253	4	US-09-320-424-11
24	229.5	13.7	177	4	US-09-105-343A-7
25	224	13.4	183	4	US-09-105-343A-8
26	183	10.9	278	4	US-08-339-214-16
27	183	10.9	278	4	US-08-339-214-26

28	182	10.9	279	4	US-08-339-214-24	Sequence 24, Appl
29	182	10.9	279	4	US-08-339-214-32	Sequence 32, Appl
30	173.5	10.4	281	4	US-08-810-453-2	Sequence 2, Appl
31	173.5	10.4	281	3	US-08-815-190A-2	Sequence 2, Appl
32	173.5	10.4	281	4	US-09-290-640-25	Sequence 25, Appl
33	173.5	10.4	281	4	US-09-479-524-3	Sequence 3, Appl
34	173.5	10.4	281	4	US-08-339-214-8	Sequence 30, Appl
35	173.5	10.4	281	4	US-08-339-214-30	Sequence 2, Appl
36	173.5	10.4	281	5	PCT-US95-00362-2	Sequence 2, Appl
37	171.5	10.2	261	1	US-07-940-605A-2	Sequence 8, Appl
38	171.5	10.2	261	1	US-08-184-422-8	Sequence 2, Appl
39	171.5	10.2	261	1	US-08-360-923A-2	Sequence 2, Appl
40	171.5	10.2	261	1	US-08-446-922-4	Sequence 4, Appl
41	171.5	10.2	261	2	US-08-431-055-4	Sequence 4, Appl
42	171.5	10.2	261	2	US-08-690-096-2	Sequence 2, Appl
43	171.5	10.2	261	2	US-08-249-189-12	Sequence 12, Appl
44	171.5	10.2	261	2	US-08-484-624A-12	Sequence 12, Appl
45	171.5	10.2	261	2	US-08-477-733B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-842-7

Query Match	100.0%;	Score 1675;	DB 2;	Length 316;
Best Local Similarity	100.0%;	Pred. No. 2.9e-157;		
Matches 316;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MRRASRDYGYLRSSEMGSGPGVPHGCPHLPAPSAPAPPPAAASRSMFLALLGLGLGQ	60	
Db	1	MRRASRDYGYLRSSEMGSGPGVPHGCPHLPAPSAPAPPPAAASRSMFLALLGLGLGQ	60	
QY	61	VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ	120	
Db	61	VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ	120	
QY	121	AFQGAQVKELQHVIGPQRFSGAPAMMEGSWLDVAQRKPEAQFFAHLTINAASIPSGSHK	180	

Db 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFAHLTINAAIPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
Db 241 VVKTSIKIPSSHNLMKGGSTKNWGSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316

RESULT 2
US-08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Mattson, Jeanine D.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; TITLE OF INVENTION: Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-362-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.9e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKLRSEEMSGPGVPEHGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYGYKLRSEEMSGPGVPEHGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLSEDTLPDSCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLSEDTLPDSCRRMKQ 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFAHLTINAAIPSGSHK 180
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFAHLTINAAIPSGSHK 180

Db 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFAHLTINAAIPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
Db 241 VVKTSIKIPSSHNLMKGGSTKNWGSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316

RESULT 3
US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mouse
US-09-052-521C-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.9e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKLRSEEMSGPGVPEHGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYGYKLRSEEMSGPGVPEHGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLSEDTLPDSCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLSEDTLPDSCRRMKQ 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFAHLTINAAIPSGSHK 180
Db 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFAHLTINAAIPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
Db 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
Db 241 VVKTSIKIPSSHNLMKGGSTKNWGSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316

RESULT 4
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:

;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/996,139
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 294 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-996-139-11

Query Match 92.8%; Score 1554; DB 3; Length 294;
Best Local Similarity 99.7%; Pred. No. 2.3e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 GVPHEGLHPAPSAPAPAPPPAASRSMTALLGLGQVVCSTALFLYFRAQMDPNRISE 82
Db 1 GVPHEGLHPAPSAPAPAPPPAASRSMTALLGLGQVVCSTALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENAGLDSTLESEDTPDSCRRMKQAFQAVOKELQHVGPORFSGA 142
Db 61 DSTHCFYRILRLHENAGLDSTLESEDTPDSCRRMKQAFQAVOKELQHVGPORFSGA 120
QY 143 PAMMEGSLDVAQRGKPEAQPFPAHLTINAASTPSGSHKVTLSWYHDRGWAKISNMTLSN 202
Db 121 PAMMEGSLDVAQRGKPEAQPFPAHLTINAASTPSGSHKVTLSWYHDRGWAKISNMTLSN 180
QY 203 GKLRVNDQGFYLYLANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKN 262
Db 181 GKLRVNDQGFYLYLANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKN 240
QY 263 WSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSSLDDPDQDATYFGAFKQVQDID 316
Db 241 WSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSSLDDPDQDATYFGAFKQVQDID 294
RESULT 5
US-08-995-659-11

;; Sequence 11, Application US/08995659
;; Patent No. 6242213
;; GENERAL INFORMATION:
;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/995,659
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 294 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-995-659-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 2.3e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 GVPHEGLHPAPSAPAPAPPPAASRSMTALLGLGQVVCSTALFLYFRAQMDPNRISE 82
Db 1 GVPHEGLHPAPSAPAPAPPPAASRSMTALLGLGQVVCSTALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENAGLDSTLESEDTPDSCRRMKQAFQAVOKELQHVGPORFSGA 142
Db 61 DSTHCFYRILRLHENAGLDSTLESEDTPDSCRRMKQAFQAVOKELQHVGPORFSGA 120
QY 143 PAMMEGSLDVAQRGKPEAQPFPAHLTINAASTPSGSHKVTLSWYHDRGWAKISNMTLSN 202
Db 121 PAMMEGSLDVAQRGKPEAQPFPAHLTINAASTPSGSHKVTLSWYHDRGWAKISNMTLSN 180
QY 203 GKLRVNDQGFYLYLANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKN 262
Db 181 GKLRVNDQGFYLYLANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKN 240
QY 263 WSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSSLDDPDQDATYFGAFKQVQDID 316

Db 241 WSGNSEHFYSINVGFFKLRAGEEISIQVNSPILDDPDQDATYFGAFKVQDID 294
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RESULT 6
US-09-215-649A-11
; Sequence 11, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 2.3e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 GVPHEGLHPAPAPAPAPPAASRSMLALLGLGLGVVCSIALFLYFRAQMDPNRISE 82
|||||
Db 1 GVPHEGLHPAPAPAPAPPAASRSMLALLGLGLGVVCSIALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRLRLHENAGLDSTLESDTLPDCRRMKQAFQAVQKELQHIYGPORFSGA 142
|||||
Db 61 DSTHCFYRLRLHENAGLDSTLESDTLPDCRRMKQAFQAVQKELQHIYGPORFSGA 120
QY 143 PAMMEGSLDVAQKGPKEAQPFAHLTINAASTIPSGSHKVTLSWYHDSWAKISNMTLSN 202
|||||
Db 121 PAMMEGSLDVAQKGPKEAQPFAHLTINAASTIPSGSHKVTLSWYHDSWAKISNMTLSN 180
QY 203 GKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
|||||
Db 181 GKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240

QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVNSPILDDPDQDATYFGAFKVQDID 316
|||||
Db 241 WSGNSEHFYSINVGFFKLRAGEEISIQVNSPILDDPDQDATYFGAFKVQDID 294
|||||
RESULT 7
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-139-13

Query Match 84.6%; Score 1417.5; DB 3; Length 317;
Best Local Similarity 84.3%; Pred. No. 7.4e-132;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
QY 1 MRRASRDYKYLRSSEMGSGPGVPHGPHLPAPAPAPAPPAASRSMLALLGLGLGQ 60
|||||
Db 1 MRRASRDYKYLRSSEMGSGPGVPHGPHLPAPAPAPPAASRSMLALLGLGLGQ 59
QY 61 VVCSIALFLYFRAQMDPNRISEDTSTHCFYRLRLHENAGLDSTLESDT--LPDSCRM 118
|||||
Db 60 VVCSVALFFYFRAQMDPNRISEDTSTHCFYRLRLHENAGLDSTLESDTKLIPDCRRI 119
QY 119 KQAFQAVQKELQHIYGPORFSGAPAMMEGSLDVAQKGPKEAQPFAHLTINAASTIPSGS 178
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Db 120 KQAFQAVQKELQHIYGPORFSGAPAMMEGSLDVAQKGPKEAQPFAHLTINAASTIPSGS 179

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QY 179 HKYTLSSWTHDRGAWAKISNMWTSNGKLRVNQDGFYYLYYANICFRHHETSGSVPTDYLQLM 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HKVLSLSSWTHDRGAWAKISNMWTSFSGKLIYNQDGFYYLYYANICFRHHETSGDLATEYLQLM 239
QY 239 VYVYKTSIKTPSSHNLKMGSGTKNWSGSEFFHYSINVGGFFKLKLRAGEEISIQVSNPSSL 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 VYVYKTSIKTPSSHTLMKGSTKYWGNSEFFHYSINVGGFFKLKLRSGEEISIEVSNPSSL 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 DPQDQATYFGAFKVDID 316
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 DPQDQATYFGAFKVRDID 317
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RESULT 8
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-13

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
Best Local Similarity 84.3%; Pred. No. 7.4e-132;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps
QY 1 MRRASRDYGYKLYRSSEMGSGGVPHPGPHLPAPSAPAPPPAASRSFMFLALLGLGLGQ 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 7.4e-132;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYLRSSEMGSGPGVHPEGPLHPAPSAPAPPPAASRSMFALLGLGLGQ 60
 DB 1 MRRASRDYTYLKGSEMGSGPGAPHEGPLH-APPPAPHQPPAASRSMFALLGLGLGQ 59
 QY 61 VVCSIALFLYFRAQMDPNRISEDTSTHCFYRILRLHFNAGLDSTLESDT--LPDSCRRM 118
 DB 60 VVCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHFNADFDQTTLESQDTKLIPDSCRR 119
 QY 119 KQAFQAVQELQHIHVCPQRFSGAPAMWEGSWLDVAQRGKPEAOPFAHLTINAASIPSGS 178
 DB 120 KQAFQAVQELQHIHVGSQHIAEAKAMVDGWSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
 QY 179 HKYTLSSWYHDRGWAKISNMTLSNGKLRVNODGFYILYANICFRHHETSGSVPTDYLOLM 238
 DB 180 HKVSLSSWYHDRGWAKISNMTFSGKLRVNODGFYILYANICFRHHETSGDLATEYLQLM 239
 QY 239 VYVVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGGFKLRAGEEISIQVSNPSLL 298
 DB 240 VYVVKTSIKIPSSHTLMKGGSTKYWGNSEPHFYSINVGGFKLRSGEEISIEVSNPSLL 299
 QY 299 DPQDQATYFGAFKVDID 316
 DB 300 DPQDQATYFGAFKVRDID 317

RESULT 10
 US-09-052-521C-4
 ; Sequence 4, Application US/09052521C
 ; Patent No. 6316408
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 ; FILE REFERENCES: A-451Bv
 ; CURRENT APPLICATION NUMBER: US/09/052,521C
 ; CURRENT FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 08/880,855
 ; PRIOR FILING DATE: 1997-06-23
 ; PRIOR APPLICATION NUMBER: 08/842,842
 ; PRIOR FILING DATE: 1997-04-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-052-521C-4

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 7.4e-132;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYLRSSEMGSGPGVHPEGPLHPAPSAPAPPPAASRSMFALLGLGLGQ 60
 DB 1 MRRASRDYTYLKGSEMGSGPGAPHEGPLH-APPPAPHQPPAASRSMFALLGLGLGQ 59
 QY 61 VVCSIALFLYFRAQMDPNRISEDTSTHCFYRILRLHFNAGLDSTLESDT--LPDSCRRM 118
 DB 60 VVCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHFNADFDQTTLESQDTKLIPDSCRR 119
 QY 119 KQAFQAVQELQHIHVCPQRFSGAPAMWEGSWLDVAQRGKPEAOPFAHLTINAASIPSGS 178
 DB 120 KQAFQAVQELQHIHVGSQHIAEAKAMVDGWSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
 QY 179 HKYTLSSWYHDRGWAKISNMTLSNGKLRVNODGFYILYANICFRHHETSGSVPTDYLOLM 238
 DB 180 HKVSLSSWYHDRGWAKISNMTFSGKLRVNODGFYILYANICFRHHETSGDLATEYLQLM 239
 QY 239 VYVVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGGFKLRAGEEISIQVSNPSLL 298

Db	240	YVYTKSIKIPSSHTLMKGGSTKYWSNGSEHFYSINVGFFKLRSGGEISIEVSNPSLL	299
Qy	299	DPDQDATYFGAFKVQDID	316
Db	300	DPDQDATYFGAFKVRDID	317
RESULT 11			
US-09-072-993C-3			
; Sequence 3, Application US/09072993C			
; Patent No. 6346388			
; GENERAL INFORMATION:			
; APPLICANT: Michael R. Brigham-Burke			
; APPLICANT: Peter R. Young			
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND			
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS			
; FILE REFERENCE: GH-50030			
; CURRENT APPLICATION NUMBER: US/09/072,993C			
; CURRENT FILING DATE: 1998-05-06			
; PRIOR APPLICATION NUMBER: 60/055,513			
; PRIOR FILING DATE: 1997-08-13			
; PRIOR APPLICATION NUMBER: 60/056,980			
; PRIOR FILING DATE: 1997-08-26			
; PRIOR APPLICATION NUMBER: 60/057,550			
; PRIOR FILING DATE: 1997-08-29			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 3			
; LENGTH: 279			
; TYPE: PRT			
; ORGANISM: HOMO SAPIENS			
US-09-072-993C-3			
Query Match 15.4%; Score 258.5; DB 4; Length 279;			
Best Local Similarity 26.4%; Pred. No. 1.3e-17;			
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps			
Qy	43	PAASRSMFLALIGLIGGVVCSIALFLYRAQMD--PNRISEDSHTCFYRLRHHENAGL	100
Db	8	PSLGQTCVLIVFTVFLQLSLCVAVTVYFTNELKQMDKYSGIACF-----LKEDDSY	62
Qy	101	QDSTLESEDTLPDSCRMKAQFQAVQK-----ELQHVGVQRFSGAPAM	146
Db	63	WDP--NDESMNSPCQVKKQLRQLRVRLRSEETISTVQEKQNI SPL-----	111
Qy	147	EGSWLDVAQRKQPEAQFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS	196
Db	112	-----VRERGQPQVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS	163
Qy	197	NWTLNCKLRVNQDGFYLLYANICFRHHETSGSVPTDYQLQWVYVVKTSIKIPSSHNLMK	256
Db	164	NLHRUNELVTHEKGFYIYSQTVFQBEIKENTKNDKQMYIYKYT--SYDPDILLMK	222
Qy	257	GGSTKNMGSNEHFYSINVGFFKLRAGEISIQVSNPSLLDPDQDATYFGAFKV	312
Db	223	SARNCSWKADEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASEFFGAFV	278
RESULT 12			
US-08-670-354-2			
; Sequence 2, Application US/08670354			
; Patent No. 5763223			
; GENERAL INFORMATION:			
; APPLICANT: Steven R. Wiley and			
; APPLICANT: Raymond G. Goodwin.			
; TITLE OF INVENTION: Cytokine That Induces Apoptosis			
; NUMBER OF SEQUENCES: 9			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation			
; STREET: 51 University Street			
; CITY: Seattle			

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; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-670-354-2

Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.4e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRMFLALGLGLGVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
Db 10 PSLGOTCVLIVITVLLQSLCVAVTYVFTNELKQMDKYSKSGIACF-----LKEDDSY 64
QY 101 QDSTLESDTLPDCRRMKAFQGVOK-----ELQHVIGPQRFSGAPAMM 146
Db 65 WDP--NDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPL----- 113
QY 147 EGSWLDVAQRGKPEAQPFALHT-----INAAISPGSHKVTL-----SSWYHDR-GWAKIS 196
Db 114 -----VREGRQORVA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSL 165
QY 197 NMTLSNGKLRVNDQGFYLYANICFRHETSGSVPTDYQLMIVYVVKTSIKIPSSHNLMK 256
Db 166 NLHLRNGELVIEHKGFIYISQTYFRQEIEKENTKNDKQMVQYIYKYT-SYPDPILLMK 224
QY 257 GGSTKNWGSNFEHFSYINVGGFFKLAGEEISIQVSNPSLLDDPDQATYFGAFKV 312
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 13
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-584-031-1

Query Match 15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.4e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRMFLALGLGLGVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
Db 10 PSLGOTCVLIVITVLLQSLCVAVTYVFTNELKQMDKYSKSGIACF-----LKEDDSY 64
QY 101 QDSTLESDTLPDCRRMKAFQGVOK-----ELQHVIGPQRFSGAPAMM 146
Db 65 WDP--NDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPL----- 113
QY 147 EGSWLDVAQRGKPEAQPFALHT-----INAAISPGSHKVTL-----SSWYHDR-GWAKIS 196
Db 114 -----VREGRQORVA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSL 165
QY 197 NMTLSNGKLRVNDQGFYLYANICFRHETSGSVPTDYQLMIVYVVKTSIKIPSSHNLMK 256
Db 166 NLHLRNGELVIEHKGFIYISQTYFRQEIEKENTKNDKQMVQYIYKYT-SYPDPILLMK 224
QY 257 GGSTKNWGSNFEHFSYINVGGFFKLAGEEISIQVSNPSLLDDPDQATYFGAFKV 312
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 14
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-780-496-1
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Query Match      15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.4e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRSFLLALLGLGQGVVCSIALFYFRAQMD--PNRISDSTHCFYRLRLHENAAGL 100
Db 10 PSLGQTCVLIVITVLLQSLCAVATYYFFNELKQMDKYSKSGIACF-----LKEDDSY 64
QY 101 QDSTLSESDLPDSCRRMKQAQFQAVOK-----ELQHVIGVPORFSGAPAMM 146
Db 65 WDP--NDEESMNSPCWQVKKWQLROLVRKMLIRTSEETISTVQERKQONISPL----- 113
QY 147 EGSWLDVAQGRKPEAQPFAPHLT-----INAAISPGSSHKYTL-----SSWYHDR-GWAKIS 196
Db 114 -----VRERGQORVA--AHITGTRGSNTLSSPNSKNEKALGRKINSWESSRGHSHSFLS 165
QY 197 NMTLSNGKLKRVNDGDFYLLYANICFRIHETSGSVPTDYQLQLVVVVVTSTIKIPSSHNLMK 256
Db 166 NLHLRNGELVIEHKGFFYYIYSQTVRFQEEIKENTKNDKQMVQIYKYT-SYDPDILLMK 224
257 GGSTKNWGSNRFHYSVINGGPFKLRAGEISIQVNSPLDDPDQDQATYTGAPKV 312
Db 225 SARNSCWSDAEGYGLXSIYQGGIFELKENDRIFYSVTNEHLIDMDHEASFQGAFLV 280

RESULT 15
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poremski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134. US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

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Query Match	15.4%	Score 258.5;	DB 4;	Length 281;
Best Local Similarity	26.4%	Pred. No. 1:4e-17;		

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Matches   78: Conservative    54: Mismatches 113: Indels    51: Gaps    10:
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Qy 43 PAASRSMFLALLGLGQVVCSTALFYFRAQMD--PNRISEDTSCFYRILRLHENAGL 100
| : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : :
Db 10 PSLGOTCVLIWITVLQLSCLVAVTYYFTNELKQMOKYKSIGIACF-----LKEDDSY 64

Qy 101 QDSTLESEDTPDSCRMMKAQFCQAVOK-----ELQHIVGPQRFSQPAMM 146
| : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 65 WDP--NDEESMNSPCWKKWLQRLVRKMILRTSEETISTVQEQQNISPL----- 113

Qy 147 EGSWLDYAQRKPCEAPFAHLT-----INAAISPGSHKVTL----SSWYHDR-GWAKIS 196
|| : || : || : || : || : || : || : || : || : || : || : || : || :
Db 114 -----YRERGQORVA--AHITGRGRSNLTSSPNSKNEALKGRKINSWESSRGHSFLS 165

Qy 197 NMTLSNGKLRVNDGFFYLKYANTICFRHHTSGSVPTDYLLQMYVVVKTSIKIPSSNNLMK 256
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 166 NLHLRNGELVTHEKGFFYYIYSQTIFYRFEQEEIKENTKDQKWQVIYKYT-SYPDPILLMK 224

Qy 257 GGSTKNWSGNSEPHFYISNVGGFPFKLRAGEEISIQVSNPSLLDDPDODATVFAGFV 312
|| : || : || : || : || : || : || : || : || : || : || : || : || :
Db 225 SARNSCWSKDAEYGLSYIOGGIFELKENDRIFVSVTNEHLIDWDHEASPFGAFLV 280

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Job time: 22 sec

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Job time: 22 sec

RESULT 15
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POEMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 6171787e
US-08-883-086-10

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OM protein - protein search, using sw model

Run on: July 15, 2002, 11:01:05 ; Search time 30.12 Seconds
(without alignments)
1165.316 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYKILRSSENGS.....LLDPDODATYFGAFKQVODID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL/cgcdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	1675	100.0	316	19	AAW83194	Human osteoprotege	
2	1675	100.0	316	19	AAW83017	Osteoclastogenesis	
3	1675	100.0	316	19	AAW59654	Amino acid sequenc	
4	1675	100.0	316	20	AAV17874	Murine TRANCE. Mu	
5	1675	100.0	316	21	AAV91024	Mouse OBM protein	
6	1675	100.0	316	21	AAV84418	Amino acid sequenc	
7	1675	100.0	316	21	AAV84419	Amino acid sequenc	
8	1597	95.3	318	22	AAW82092	Rat osteoclast dif	
9	1554	92.8	294	19	AAW69956	NF-kB receptor act	
10	1554	92.8	294	19	AAW68292	NF-kB receptor act	
11	1554	92.8	294	22	AAW08737	Murine receptor ac	

12	1554	92.8	294	22	AAE04425	Murine receptor ac
13	1554	92.8	294	22	AAE01992	Murine RANKL (rece
14	1554	92.8	294	22	AAE01992	Human osteoprotege
15	1417.5	84.6	317	19	AAW83195	NF-kB receptor act
16	1417.5	84.6	317	19	AAW69957	NF-kB receptor act
17	1417.5	84.6	317	21	AAW86293	Amino acid sequenc
18	1417.5	84.6	317	21	AAW84417	Human receptor act
19	1417.5	84.6	317	22	AAE08738	Human receptor act
20	1417.5	84.6	317	22	AAE04426	Human full-length
21	1409.5	84.1	317	19	AAW83018	Osteoclastogenesis
22	1318	78.7	501	22	AAE01993	Amino acid sequenc
23	1297	77.4	244	19	AAW83019	A murine OCIF-bind
24	1107	66.1	246	19	AAW83020	Osteoclastogenesis
25	1101	65.7	245	20	AAW17873	Human TRANCE. Hom
26	855	51.0	160	21	AAW08272	Amino acid sequenc
27	852	50.9	173	21	AAW84421	Amino acid sequenc
28	842	50.3	173	21	AAW84420	A murine osteoprot
29	842	50.3	173	21	AAW84422	Mouse FLAG-murine
30	830	49.6	170	22	AAW08386	An osteoprotegerin
31	804.5	48.0	188	21	AAW84423	An osteoprotegerin
32	794.5	47.4	182	21	AAW84424	An osteoprotegerin
33	771	46.0	173	21	AAW84425	DNA encoding osteo
34	768	45.9	160	21	AAW08273	Amino acid sequenc
35	746	44.5	139	21	AAW91023	Mouse OBM protein
36	741	44.2	152	22	AAW67248	Human RANKL. Homo
37	732	43.7	173	21	AAW84426	An osteoprotegerin
38	737	43.1	74	21	AAW91020	Mouse OBM protein
39	285	17.0	54	21	AAW91021	Mouse OBM protein
40	259.5	15.5	281	20	AAW27016	Human Apo-2 ligand
41	259.5	15.5	281	20	AAW27017	Human Apo-2 ligand
42	258.5	15.4	279	19	AAW76332	Human TL2 (TRAIL),
43	258.5	15.4	279	20	AAW95032	Tumour necrosis fa
44	258.5	15.4	281	18	AAW27134	Human Apoptosis in
45	258.5	15.4	281	18	AAW19787	Human apoptosis in

ALIGNMENTS

RESULT 1

AAW83194

ID AAW83194 standard; Protein; 316 AA.

XX AAC

XX AAW83194;

DT 11-FEB-1999 (first entry)

XX

DE Human osteoprotegerin binding protein from the 32D-F3 ins.

XX

DE Human; osteoprotegerin binding protein; OPB binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease.

XX

OS Homo sapiens.

XX

PN W09846751-Al.

XX

PD 22-OCT-1998.

XX

XX 15-APR-1998; 98WO-US07584.

XX

PR 30-MAR-1998; 98US-0052521.

XX

PR 16-APR-1997; 97US-0842842.

XX

PR 23-JUN-1997; 97US-0880855.

XX

XX (AMGE-) AMGEN INC.

XX

XX Boyle WT;

PI

XX WPI; 1998-594578/50.

DR N-PSDB; AAV70284.

XX

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX
XX Claim 19; Fig 1; 47pp; English.
XX
XX The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX
XX Sequence 316 AA;
SQ

Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYGYKLSSEEMSGPGVPHGPHLPAPSAPAPAPPPAASRSMFLALLGLGQ 60
Db 1 mrrasrdygyklsseemsgpgvphgphlpapsapapppaasrsmflallglgq 60

Qy 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRMKQ 120
Db 61 vvcsialflyfraqmdpnrisdsthcfyrlrlhenagldstlesedtlpdscrmkq 120

Qy 121 AFOGAVQKELQHVGPORFSGAPAMMEGSLDVAQRGKPEAQPFALHTINAASIPSGSHK 180
Db 121 afggavqkelqhvpgprfsgapammegswldvaqrqkpeaqpfahltnaasipsghk 180

Qy 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
Db 181 vtlswwyhdrgwakismntlsngklrvnqdgfylyanicfrhhetsgsvptdyqlmzy 240

241 VVKTSIKIPSSHNLKMGSTKNWGSNEFHYSINVGFFKL RAGEEISIQVSNPSLLDP 300
Db 241 vvktsikipsshnlnkmgstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy 301 DQDATYFGAFKVDID 316
Db 301 dqdatyfgafkvqdid 316

RESULT 2
AAW83017
ID AAW83017 standard; Protein; 316 AA.
XX
AC AAW83017;
XX
DT 10-FEB-1999 (first entry)
XX
XX Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW Osteoclast; bone absorption factor; bone disorder; calcium metabolism.
XX
OS Unidentified.
XX

PN W09846644-A1.
XX
PD 22-OCT-1998.
XX
PF 15-APR-1998; 98WO-JP01728.
XX
XX 02-DEC-1997; 97JP-0332241.
PR 15-APR-1997; 97JP-0097808.
PR 09-JUN-1997; 97JP-0151434.
PR 12-AUG-1997; 97JP-0217897.
PR 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
PA
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI: 1998-594563/50.
DR N-PSDB; AAV69886.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
XX
XX Claim 8; Pages 106-108; 151pp; Japanese.
XX
XX The present sequence represents an osteoclastogenesis inhibitory factor
CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC separation and maturation of osteoclasts in the presence of bone
CC absorption factors such as calcitriol or parathyroid hormone (PTH).
CC OBM is isolated from stroma cells cultured in the presence of a bone
CC absorption factor by separation and solubilisation of membrane proteins
CC then affinity chromatography using OCIF. It exists in a full-sequence
CC form and a solubilised form (sOBM) which is a shorter chain. OBM may be
CC used for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
XX Sequence 316 AA;
SQ

Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYGYKLSSEEMSGPGVPHGPHLPAPSAPAPAPPPAASRSMFLALLGLGQ 60
Db 1 mrrasrdygyklsseemsgpgvphgphlpapsapapppaasrsmflallglgq 60

Qy 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRMKQ 120
Db 61 vvcsialflyfraqmdpnrisdsthcfyrlrlhenagldstlesedtlpdscrmkq 120

Qy 121 AFOGAVQKELQHVGPORFSGAPAMMEGSLDVAQRGKPEAQPFALHTINAASIPSGSHK 180
Db 121 afggavqkelqhvpgprfsgapammegswldvaqrqkpeaqpfahltnaasipsghk 180

Qy 181 VTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
Db 181 vtlswwyhdrgwakismntlsngklrvnqdgfylyanicfrhhetsgsvptdyqlmzy 240

Qy 241 VVKTSIKIPSSHNLKMGSTKNWGSNEFHYSINVGFFKL RAGEEISIQVSNPSLLDP 300
Db 241 vvktsikipsshnlnkmgstknwsgnsefhfysinvggffklrageeisiqvsnpslldp 300

Qy 301 DQDATYFGAFKVDID 316
Db 301 dqdatyfgafkvqdid 316

```
RESULT 3
AAW59654
ID AAW59654 standard; Protein; 316 AA.
XX
AC AAW59654;
XX
DT 24-SEP-1998 (first entry)
XX
DE Amino acid sequence of mouse 499E9 protein.
XX
KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW antagonist; autoimmune disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW acute inflammatory response; antibody; antigen; cancer.
XX
OS Mus sp.
XX
FH Domain 1..49
FT /note= "intracellular domain"
XX
XX W09825958-A2.
XX
XX 18-JUN-1998.
XX
XX 12-DEC-1997; 97WO-US22766.
XX
XX 13-DEC-1996; 96US-0032846.
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Mattson JD;
XX
XX WPI; 1998-348452/30.
XX N-PSDB; AAV41489.
XX
XX Mouse cell surface antigen, 499E9 protein - used to treat conditions
XX associated with abnormal physiology or development
XX
XX Claim 1; Pages 8-11; 59pp; English.
XX
XX This is the amino acid sequence of the mouse 499E9 protein, used
XX in the method of the invention to treat conditions associated with
XX abnormal physiology or development. The 499E9 protein is expressed
XX highly on polarised Th1 T cells, binding of 499E9 to its receptor may
XX result in either immune cell expansion or apoptosis. Antagonists of
XX 499E9 may be used to modulate immune responses in abnormal situations,
XX e.g. autoimmune disorders including rheumatoid arthritis, systemic
XX lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
XX acute inflammatory responses in which T-cell expansion, activation or
XX immunological T-cell memory play an important role. The antibodies
XX can be used to raise anti-idiotypic antibodies which will be useful
XX in detecting or diagnosing various immunological conditions related to
XX the expression of antigens of 499E9. The antibodies, and fragments of
XX 499E9 can be used in the treatment of conditions associated with
XX abnormal physiology or development, including abnormal proliferation
XX (e.g. cancerous conditions) or degenerative conditions.
XX
XX Sequence 316 AA;
XX
Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYKYLRSSEMGSGVPHPGPHLPAPSAPAPAPPPPAASRMFLALGLGLGQ 60
DB 1 mrrasrdygykylrssemgsgvgpvhpgpLhpapsapappppaasrmfllalglglgq 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRLRLHENAGLQDSTLESDTLDPSCRRMKQ 120
```

```
Db 61 vvcslalflyfragmdpnrisdsthcfyrlrlhenagldstlesedtlpdsrrmkq 120
QY 121 AFOGAVOKELQHVGPORFSGAPAMMEGSLDVAORGPKEAPQFAHLTINAASIPSGSHK 180
Db 121 afqgavqkelqhvqpqrfsgapammedswldvagrkgpeaqpfahltinaasipsgshk 180
QY 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLQLMY 240
Db 181 vtlsswyhdrgwakisnmtlsgklrvnqdgffyylyanicfrhshetsgsvptdyqlqlmvy 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGGFFKLRAGEEISIQVNSPLDP 300
Db 241 vvktsikipsshnlmkggstknwgnsefhfysinvggffklrageeisiqvnspldp 300
QY 301 DQDATYFGAFKVDID 316
Db 301 dqdatyfgafkvqdid 316
RESULT 4
AAV17874
ID AAV17874 standard; Protein; 316 AA.
XX
AC AAV17874;
XX
DT 17-AUG-1999 (first entry)
XX
DE Murine TRANCE.
XX
KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
KW TNF-related activation induced cytokine; immune response; cancer;
KW autoimmune disease; HIV; hypersensitivity; allergen.
XX
OS Mus musculus.
XX
XX W09929865-A2.
XX
XX 17-JUN-1999.
XX
XX 14-DEC-1998; 98WO-US26486.
XX
XX 11-DEC-1998; 98US-0989479.
XX 12-DEC-1997; 97US-0989479.
XX 03-MAR-1998; 98US-0034099.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Choi Y, Josien R, Steinman R, Won B;
XX
XX WPI; 1999-385609/32.
XX N-PSDB; AAX80224.
XX
XX TNF like proteins for treating autoimmunity and cancer
XX
XX Claim 9; Fig 3; 164pp; English.
XX
XX The present sequence represents murine TNF-related activation induced
XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX variants, fragments, derivatives or analogues may be used as modulators
XX of immune response in a mammal comprising, antisense sequences to
XX TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX Agonists and antagonists of TRANCE, can be used to modulate immune
XX response by increasing or decreasing the life span of mature dendritic
XX cells and increasing or decreasing T cell activation. These techniques
XX are especially useful for treating immune system related conditions such
XX as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX The TRANCE polypeptides can be used to increase the viability of
XX dendritic cells in vivo or in vitro, especially when used in conjunction
XX with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CD40L or TNF-alpha).
XX
XX Sequence 316 AA;
```


PR 15-SEP-1998; 98DK-0001164.
XX 02-OCT-1998; 98US-0102896.
PA (MEBI-) M & E BIOTECH AS.
XX Halkier T, Haaning J;
XX WPI; 2000-271444/23.
DR N-PSDB; AA299965.
XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT to treat, prevent and ameliorate osteoporosis -
XX Claim 17; Page 81-82; 110pp; English.
XX The present sequence represents a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
SQ Sequence 316 AA;
Query Match 100.0%; Score 1675; DB 21; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKYLRSSEMGSGVPHGPHLPAPSAPAPAPPAAASRMFLALLGLGLGQ 60
DB 1 mrrasrdygykylrsseemsgsgvphegphlpapsapapappaaasrmflallg1g1gq 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESEDTLPDSCRRMKQ 120
DB 61 vvcsialflyraqmdpnrisdsthcfyrlrlhenagldstlesedtlpdscrrmkq 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMGSLDVAQKGPKEAQPFAHLTINAAISIPSGSHK 180
DB 121 afggavqkelqhvpgqrfsgapammegswldvaqrgkpeuqpfahltinaasipsgshk 180
QY 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
DB 181 vtlsswyhdrgwakisnmtlsngklrvnqdgfylyanicfrhhetsgsvptdyqlmzy 240
QY 241 VKVTSIKIPSHNLKMGSTKNNSGNEFHFYSINVGGFFKLAGEEISIQVSNPSLLDP 300
DB 241 vkvtsikipshnlkmgstknsgnefhyfysinvggffklageeisqvsnpslldp 300
QY 301 DQDATYFGAFKVDQID 316
DB 301 dqdatyfgafkvqdid 316
RESULT 7
AY84419
ID AAY84419 standard; Protein; 316 AA.
XX AAY84419;
XX AAY84419;
XX 25-JUL-2000 (first entry)
XX Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW

KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption.
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 49..69
FT /note= "transmembrane region"
FT Domain 70..157
FT /note= "extracellular stalk domain"
FT Region 158..317
FT /note= "active ligand moiety"
XX WO200015807-A1.
XX 23-MAR-2000.
XX 13-SEP-1999; 99WO-DK00481.
XX 15-SEP-1998; 98DK-0001164.
XX 02-OCT-1998; 98US-0102896.
XX (MEBI-) M & E BIOTECH AS.
XX Halkier T, Haaning J;
XX WPI; 2000-271444/23.
XX N-PSDB; AA299966.
XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX to treat, prevent and ameliorate osteoporosis -
XX Claim 17; Page 85-86; 110pp; English.
XX The present sequence represents a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
SQ Sequence 316 AA;
Query Match 100.0%; Score 1675; DB 21; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYKYLRSSEMGSGVPHGPHLPAPSAPAPAPPAAASRMFLALLGLGLGQ 60
DB 1 mrrasrdygykylrsseemsgsgvphegphlpapsapapappaaasrmflallg1g1gq 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESEDTLPDSCRRMKQ 120
DB 61 vvcsialflyraqmdpnrisdsthcfyrlrlhenagldstlesedtlpdscrrmkq 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMGSLDVAQKGPKEAQPFAHLTINAAISIPSGSHK 180
DB 121 afggavqkelqhvpgqrfsgapammegswldvaqrgkpeuqpfahltinaasipsgshk 180
QY 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYQLMZY 240
DB 181 vtlsswyhdrgwakisnmtlsngklrvnqdgfylyanicfrhhetsgsvptdyqlmzy 240

Qy 241 VVKTSIKIPSSHNLMKGGSTKNWGSNRFHFYSINVGGFFKL RAGEEISIOVSNPSSLDP 300
|||||
Db 241 vvktsiklpsshnlmkgstknwgsnrfhfysinvggffklrageeisiovsnpsslldp 300
Qy 301 DQDATYFGAFKVDID 316
|||||
Db 301 dqdatyfgafkvqdid 316
RESULT 8
ID AAB82092
XX AAB82092 standard; Protein; 318 AA.
AC AAB82092;
XX
XX 29-JUN-2001 (first entry)
XX Rat osteoclast differentiation factor, ODF.
XX Rat; osteoclast formation inducer; vaccine; gene therapy;
XX Osteoclast Differentiation Factor; bone.
OS Rattus sp.
XX WO200123549-A1.
XX
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-AU01202.
XX 29-SEP-1999; 99AU-0003147.
XX (UYWA-) UNIV WESTERN AUSTRALIA.
XX
XX Xu J, Zheng M;
PI
XX WPI; 2001-335526/35.
XX N-PSDB; AAF86481.
XX
XX Novel nucleic acid encoding rat osteoclast differentiation factor
XX useful for modulating activity of a cell, e.g., cell proliferation,
XX cell differentiation and cell viability -
XX
XX Claim 5; Fig 2; 8lpp; English.
XX
XX The present sequence is the protein sequence for rat Osteoclast
XX Differentiation Factor (ODF). ODF is thought to be directly involved in
XX the differentiation of monocytes/macrophages into osteoclasts.
XX Osteoclasts promote dissolution of the bone matrix and solubilisation of
XX bone salts. The ODF coding sequence is useful in gene therapy, and as
XX hybridisation probes or primers. ODF protein is useful for modulating the
XX activity of cells, e.g., cell proliferation, cell differentiation and
XX cell viability, as immunogens to generate anti-rat ODF antibodies, and
XX as vaccines. Anti-rat ODF antibodies are useful in assay methods for
XX quantifying ODF polypeptides.
XX
SQ Sequence 318 AA;

Query Match 95.3%; Score 1597; DB 22; Length 318;
Best Local Similarity 95.0%; Pred. No. 2.5e-136;
Matches 302; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 1 MRRASRDYGYKLYRSSEMGSGPGVPEHGPLHPAPSAPAPPPAASRSMFLALLGLGQ 60
|||||
Db 1 mrrardygkylrseemgscpgvphegplhpapsapapppaasrsmflallg19l9q 60

Qy 61 VVCSIALFLYFRQADPNRISDSTHCFYRILRLHENAGLQDSTLSEPT--LPDSCRRM 118
|||||
Db 61 vvcsialflyfrqadpnrisedstcrfyrilrlentglqdstlesedtealpdscrm 120

Qy 119 KQAFGAVQKELQHVGPORFSGAPAMMEGSLDVAQKGPAPQPAHUTINAASTPSGS 178
|||||

Db 121 kqafgavqrelqhvqpqrfsqvpammegswldvarrgkpeaqpfahltnaadipsqs 180
Qy 179 HKVTLSWSWHDRAWAKISNNMTLSNGKLVRNQDGFYLYANICRPHHETSSVPTDYQLM 238
|||||
Db 181 hkvtlswwyhdrgwakisnmtlsngklvrnqdgfylyanicrhhetsgvpadyqlm 240
Qy 239 VYVVKTSIKIPSSHNLMKGGSTKNWGSNRFHFYSINVGGFFKL RAGEEISIOVSNPSSL 298
|||||
Db 241 vyvvtksiklpsshnlmkgstknwgsnrfhfysinvggffklrageeisiovsnpssll 300
Qy 299 DPDDATYFGAFKVDID 316
|||||
Db 301 dpdqtyfgafkvqdid 318
RESULT 9
AAW69956
ID AAW69956 standard; Protein; 294 AA.
XX
AC AAW69956;
XX
XX 08-OCT-1998 (first entry)
XX NF-kB receptor activator RANK ligand (RANKL).
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX immune response; inflammatory response; toxic shock; sepsis;
XX RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.
XX Mus musculus.
XX
XX WO9828426-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23775.
XX
XX 14-OCT-1997; 97US-0064571.
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0813509.
XX (IMMV) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
PI
XX WPI; 1998-377657/32.
XX N-PSDB; AAV41377.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
XX develop products for augmenting an immune response for inhibiting an
XX inflammatory response and for protection of cells
XX
XX Claim 27; Pages 55-57; 80pp; English.
XX
XX This represents a murine RANKL, a ligand for the RANK (receptor
XX activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
XX member of the tumour necrosis factor (TNF) family. A soluble RANK
XX may be used for inhibiting activation of NF-kB, by contacting a cell
XX expressing membrane-associated RANK with a soluble RANK which binds to
XX RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
XX used to induce maturation of dendritic cells and enhance their
XX allo-stimulatory capacity, thereby augmenting an immune response. The
XX soluble RANK polypeptide composition may also be used for regulating an
XX immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
XX may be useful in ameliorating negative effects of an inflammatory
XX response that result from triggering of RANK, e.g. in treating toxic
XX shock or sepsis, graft-versus-host reactions, or acute inflammatory
XX reactions. They can also be used in adjunct therapy for disease
XX characterised by neoplastic cells that express RANK. RANKL polypeptides
XX can also be used to identify inhibitors of RANK and thus inhibitors of
XX an inflammatory response, and also for protecting RANK-expressing cells
XX from the negative effects of chemotherapy or the presence of high levels
XX of TNF-alpha. The products can also be used for detection and drug

CC screening.
XX Sequence 294 AA;
SQ

Query Match 92.8%; Score 1554; DB 19; Length 294;
Best Local Similarity 99.7%; Pred. No. 1.8e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGPHAPAPAPAPPAAASRSMFLALGLGLGVVCSIALFLYFRAQMDPNRISE 82
|||||
DB 1 gvpheplhpapapapappaaasrsmflalglglgvvcsialflyfraqmdpnrise 60
|||||

QY 83 DSTHCFYRILRHENAGLDSTLESEDTLPDSCRMRKQAFQAVQKELQHIVGPORFSGA 142
|||||
DB 61 dsthcfyrlrlhenadlqdstlesedtlpdsccrmkqafgavqkelqhivgqrfsga 120
|||||

QY 143 PAMMEGSLWDVAQRKPEAQPFALHTINAAISPGSSHKVTLSSWYHGRGAKISNMILSN 202
|||||
DB 121 pammegswldvaqrkpeaqpfahltinaasipsgshkvtlsswyhgrgwakisnmtilsn 180
|||||

QY 203 GKLRVNQDGFYLYANICFRHHETSGSVPTDYQLQLMVYVVKTSIKIPSSHNLKMGSTKN 262
|||||
DB 181 gklrvnqdgfylyanicfrhhetsgsvptdyqlqlmvyvvtksikipsshnlmkggstkn 240
|||||

QY 263 WSGNSEFHYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
|||||
DB 241 wsgnsefhysinvggfkllrageeisiqvsnpslldpdqdatyfgafkvqdid 294
|||||

RESULT 10
AAW68292
ID AAW68292 standard; Protein; 294 AA.
XX
AC AAW68292;
XX
DT 08-OCT-1998 (first entry)
DE
DE NF-KB receptor activator RANK ligand (RANKL).
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.
XX
OS Mus musculus.
XX
XX WO9828424-A2.
PN

02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-US23866.
XX
XX 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Anderson DM, Gallibert LJ, Maraskovsky E;
PI
XX WPI; 1998-377655/32.
DR N-PSDB; AAV41371.
DR
XX
PT New isolated receptor activator of necrosis factor-kappa B - useful
PT for, e.g. developing products for regulating an immune or
PT inflammatory response, treating toxic shock or sepsis
XX
XX Example 7; Pages 55-57; 80pp; English.
PS
XX This represents a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. Host cells transformed
CC or transfected with an expression vector comprising the RANK encoding

CC nucleic acid can be used to produce recombinant RANK protein. The soluble
CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC used for regulating an immune or inflammatory response. Inhibition of
CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC of an inflammatory response that result from triggering of RANK, e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC inflammatory reactions. They can also be used in adjunct therapy for
CC disease characterised by neoplastic cells that express RANK. The products
CC can also be used for detection and drug screening.
XX
SQ Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 19; Length 294;
Best Local Similarity 99.7%; Pred. No. 1.8e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGPHAPAPAPAPPAAASRSMFLALGLGLGVVCSIALFLYFRAQMDPNRISE 82
|||||
DB 1 gvpheplhpapapapappaaasrsmflalglglgvvcsialflyfraqmdpnrise 60
|||||

QY 83 DSTHCFYRILRHENAGLDSTLESEDTLPDSCRMRKQAFQAVQKELQHIVGPORFSGA 142
|||||
DB 61 dsthcfyrlrlhenadlqdstlesedtlpdsccrmkqafgavqkelqhivgqrfsga 120
|||||

QY 143 PAMMEGSLWDVAQRKPEAQPFALHTINAAISPGSSHKVTLSSWYHGRGAKISNMILSN 202
|||||
DB 121 pammegswldvaqrkpeaqpfahltinaasipsgshkvtlsswyhgrgwakisnmtilsn 180
|||||

QY 203 GKLRVNQDGFYLYANICFRHHETSGSVPTDYQLQLMVYVVKTSIKIPSSHNLKMGSTKN 262
|||||
DB 181 gklrvnqdgfylyanicfrhhetsgsvptdyqlqlmvyvvtksikipsshnlmkggstkn 240
|||||

QY 263 WSGNSEFHYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
|||||
DB 241 wsgnsefhysinvggfkllrageeisiqvsnpslldpdqdatyfgafkvqdid 294
|||||

RESULT 11
AAE08737
ID AAE08737 standard; Protein; 294 AA.
XX
AC AAE08737;
XX
DT 15-NOV-2001 (first entry)
DE
DE Murine receptor activator of NF kappaB ligand (RANKL) protein.
XX
XX Murine; receptor activator of nuclear factor kappaB ligand; RANKL; NF;
KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
KW immune response; inflammatory response; graft-versus-host reaction;
KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
XX
OS Mus musculus.
XX
XX US6271349-B1.
PN
XX
XX 07-AUG-2001.
PD
XX
XX 17-DEC-1998; 98US-0215649.
PF
XX 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0772330.
PR 07-MAR-1997; 97US-0813509.
PR 22-DEC-1997; 97US-0996139.
XX
XX (IMMV) IMMUNEX CORP.
XX

PI Dougall WC, Galibert L;
XX WPI: 2001-520313/57.
DR N-PSDB: AAD13310.
XX
PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for
PT regulating immune response, in screening for RANK inhibitors, or as an
PT adjunct therapy for disease characterized by neoplastic cells that
PT express RANK -
XX
XX Example 15: Column 65-68; 47pp; English.
PS The patent discloses novel receptor activator of nuclear factor (NF)-
XX kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
CC of the tumour necrosis factor (TNF) receptor superfamily and associates
CC with TNF receptor associated factor (TRAF) 2 and 3 which are important
CC in the regulation of immune and inflammatory response. The receptors
CC are useful for regulating immune response and in screening for inhibitors
CC of these receptors. The cytoplasmic domain of RANK is used in developing
CC assays for inhibitors of signal transduction, e.g. for screening the
CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
CC are useful in ameliorating the negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, acute inflammatory
CC reactions and the effects of bone resorption. RANK acts as an anti-
CC apoptotic signal and rescue the cells that express RANK from apoptosis.
CC Soluble forms of the receptor are used in vivo or in vitro based
CC screening tests for agonists or antagonists of RANK activity, as
CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit
CC transduction of a signal via RANK. RANK compositions are used in the
CC development of both agonistic and antagonistic antibodies, or as an
CC adjunct therapy for disease characterised by neoplastic cells that
CC express RANK. Compounds that interfere with RANK/TRAF6 interactions
CC are useful for modulating the formation of osteoclasts from osteoclast
CC precursors and for modulating osteoclast function and activities. They
CC are used as inhibitors of diseases associated with excess bone resorption
CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
CC useful for the expression of recombinant proteins, as probes for analysis
CC of the presence or distribution of RANK transcripts, while the proteins
CC are useful in preparing kits for the detection of soluble RANK, or
CC monitor RANK-related activity. The present sequence is RANK ligand
CC (RANKL) protein from murine.
XX Sequence 294 AA;
SQ

Query Match 92.8%; Score 1554; DB 22; Length 294;
Best Local Similarity 99.7%; Pred. No. 1.8e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 23 GVPHEGLHPAPSAPAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE 82
Db 1 gvpheglhpapsapapapppaasrsmflallglgqvcslalflyfraqmdpnrise 60
Qy 83 DSTHCFYRILRHENAGLDSTLESDTLPDSCRRMKQAFQAGVQKELHIVGPQRFSGA 142
Db 61 dsthcfyrlrlrhenadlqdstlesedtlpdscrrmkqafgavqkelhivgpqrfsga 120
Qy 143 PAMMEGSLDVAQRKPEAQPFahlTINAAIPSGSHKVTLSWYHdRGWAKISNMTLSN 202
Db 121 pammeqslwldvaqrkpeaqpfahlTinaasipsgshkvltsswyhdrwkwakismntlsn 180
Qy 203 GKLRVNDQGFYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLKMGSTKN 262
Db 181 gklrvndqgfylyanicfrhethetsgsvptdyqlqmvvyvkvtsiklpsshnlmggstkn 240
Qy 263 WSGNSEFFHYSINVGGFFKLAGEISIQVSNPSLDDPDQDATYFAKFVQDID 316
Db 241 wsgnsefnyfynvggffklageisiqvsnpslldpdqdatyfaqfkdqid 294

RESULT 12

AAE04425
ID AAE04425 standard; Protein; 294 AA.
XX
AC AAE04425;
XX
DT 04-SEP-2001 (first entry)
XX
DE Murine receptor activator of NF-chi B ligand (RANKL) protein.
XX
KW Murine; receptor activator of NF-chi B; RANK; tumour necrosis factor;
KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
KW chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH Region 139..294
FT /note="Receptor binding region"
FT
PN US6242213-B1.
XX
PD 05-JUN-2001.
XX
XX 22-DEC-1997; 97US-0995659.
XX
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM;
XX
DR WPI; 2001-407216/43.
DR N-PSDB; AAD08714.
XX
PT New DNA molecules, useful for producing ligands (which are useful for
PT regulating immune response and in screening for inhibitors of NF-chi B
PT receptor activator) of the receptor activator of NF-chi B (RANK) -
XX
PS Example 7; Column 59-62; 43pp; English.
XX
CC The present invention relates to receptor activator of NF-chi B (RANK)
CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC proteins respectively. RANK is a member of the tumour necrosis factor
CC (TNF) superfamily and it closely resembles CD40 in the extracellular
CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
CC The ligands are useful for regulating immune response and in screening
CC for inhibitors of RANK. The present sequence is murine RANKL protein.
XX Sequence 294 AA;
SQ

Query Match 92.8%; Score 1554; DB 22; Length 294;
Best Local Similarity 99.7%; Pred. No. 1.8e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 23 GVPHEGLHPAPSAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE 82
Db 1 gvpheglhpapsapapppaasrsmflallglgqvcslalflyfraqmdpnrise 60
Qy 83 DSTHCFYRILRHENAGLDSTLESDTLPDSCRRMKQAFQAGVQKELHIVGPQRFSGA 142
Db 61 dsthcfyrlrlrhenadlqdstlesedtlpdscrrmkqafgavqkelhivgpqrfsga 120
Qy 143 PAMMEGSLDVAQRKPEAQPFahlTINAAIPSGSHKVTLSWYHdRGWAKISNMTLSN 202
Db 121 pammeqslwldvaqrkpeaqpfahlTinaasipsgshkvltsswyhdrwkwakismntlsn 180
Qy 203 GKLRVNDQGFYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLKMGSTKN 262
Db 181 gklrvndqgfylyanicfrhethetsgsvptdyqlqmvvyvkvtsiklpsshnlmggstkn 240

Db 181 gklrvnqdgfylylanicfrhthetgsyptdyqlmvyvvtksiklpsshnlmkggstkn 240

QY 263 WSGNSEFHYSINVGGFKLRAGEISIOVSNPSLLDPDQATYFGAKVQDID 316

Db 241 wsgnsefhysinvggfkrlageeisiqvanpslldpdqatyfgakvqdid 294

RESULT 13

AAE01992

ID AAE01992 standard; Protein; 294 AA.

XX AC AAE01992;

XX 31-JUL-2001 (first entry)

XX DE Murine RANKL (receptor activator of NF-kappaB ligand) protein.

XX KW Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;

XX KW TNF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;

XX KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;

XX KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;

XX KW immune system dysfunction; familial expansile osteolysis; FEO;

XX KW early onset Paget's disease of bone; EP; cytostatic.

XX OS Mus musculus.

XX PN WO200136637-A1.

XX PD 25-MAY-2001.

XX PF 14-NOV-2000; 2000WO-US31459.

XX PF 17-NOV-1999; 99US-0442029.

XX PR (IMMUNEX CORP.

XX PA Anderson DM, Hughes AE;

XX PI WPI; 2001-329222/34.

XX DR N-PSDB; AAD05903.

XX DR New DNA encoding a receptor activator of NF-kappaB polypeptide for the

XX PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -

XX PS Disclosure; Page 74-75; 96pp; English.

XX CC The present invention relates to a novel receptor, referred to as RANK

XX CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF

XX CC (tumour necrosis factor) receptor superfamily. RANK is a Type I

XX CC transmembrane protein that interacts with TNF receptor-associated

XX CC factors (TRAFs). Triggering of RANK by overexpression or co-expression

XX CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation

XX CC of the transcription factor NF-kappaB, a ubiquitous transcription factor

XX CC that is most extensively utilised in cells of the immune system.

XX CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating

XX CC negative effects of inflammatory reactions, and the effects of excess

XX CC bone resorption. The RANK DNAs, proteins and their analogues are useful

XX CC for the preparation of pharmaceutical compositions, for infecting target

XX CC cells for use in gene therapy applications in diagnosing diseases

XX CC associated with RANK, and as targets for use in screening assays. They

XX CC may be used in the treatment or diagnosis of immune system dysfunction.

XX CC The present invention also encompasses gene therapy methods to correct

XX CC gene-activating mutations, associated with e.g. familial expansile

XX CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The

XX CC present amino acid sequence is murine RANKL (muRANKL) protein.

XX SQ Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 22; Length 294;

Best Local Similarity 99.7%; Pred. No. 1.8e-132;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GYPHEGLHPAPSAPAPAPPAAASRSMEIALLGLGIGOVVCSIALFLYFRAOMDPNRIS 82

Db 1 gypheglhpsapapappaaasrmfiallgigqvvcslalflyfraomdpnrise 60

QY 83 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQAFQGAQVQKELQHVGPQRFSGA 142

Db 61 dsthcfyrlrlhenadlqdstlesedtlpdscrrmkqafgqavqkelqhvqpqrfsa 120

QY 143 PAMMEGSLDVAQRGKPEAQPFALHTINAASTPSGSHKVTLSWYHDRGWAKISNMTLSN 202

Db 121 pammegswldvaqrqkpeaqpfahltnaaasipsgshkvtlsswyhdrwgakisnmtlsn 180

QY 203 GKLRVNQDGFYLYLANICFRHHTSGSVPTDYQLQLMVYVVKTSIKIPSSHNLKGGSTKN 262

Db 181 gklrvnqdgfylylanicfrhthetgsyptdyqlmvyvvtksiklpsshnlmkggstkn 240

QY 263 WSGNSEFHYSINVGGFKLRAGEEISIOVSNPSLLDPDQATYFGAKVQDID 316

Db 241 wsgnsefhysinvggfkrlageeisiqvanpslldpdqatyfgakvqdid 294

RESULT 14

AAW83195

ID AAW83195 standard; Protein; 317 AA.

XX AC AAW83195;

XX DT 11-FEB-1999 (first entry)

XX DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.

XX KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;

XX KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;

XX KW hypercalcaemia; osteoclast differentiation and activation receptor;

XX KW Paget's disease.

XX OS Homo sapiens.

XX PN WO9846751-A1.

XX PD 22-OCT-1998.

XX PF 15-APR-1998; 98WO-US07584.

XX PR 30-MAR-1998; 98US-0052521.

XX PR 16-APR-1997; 97US-0842842.

XX PR 23-JUN-1997; 97US-0880855.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ;

XX WPI; 1998-594578/50.

XX N-PSDB; AAW70285.

XX PT Nucleic acid encoding osteoprotegerin binding protein - useful for

XX PT e.g. treating bone diseases by modulating osteoclast differentiation

XX PT and for diagnosis

XX PS Claim 19; Fig 4; 47pp; English.

XX CC The present sequence is human osteoprotegerin (OPG) binding protein.

XX CC Host cells transfected with vectors containing nucleic acid molecules

XX CC encoding OPG binding protein are used to produce recombinant OPG binding

XX CC protein. OPG binding protein is used in binding assays to determine

XX CC osteoprotegerin (OPG) in biological samples; to screen for specific

XX CC binding agents (particularly agonists and antagonists, including

XX CC intracellular proteins); to raise Ab (useful in immunoassays for

XX CC detection of OPG binding protein) and to identify compounds that

XX CC modulate binding of OPG binding protein to osteoclast differentiation

XX CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG

XX CC binding protein can be used to detect OPG binding protein-encoding

XX CC sequences, e.g. screening for related sequences, also to produce

CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX
SQ Sequence 317 AA;

Query Match 84.6%; Score 1417.5; DB 19; Length 317;
Best Local Similarity 84.3%; Pred. No. 4.4e-120;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYLRSEEMSGPGVHEGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 mrrasrdytkylrgseemggpgaphegplh-appppahqpapaarsmfvallglgq 59

QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLDSTLESDT--LPDSCRMM 118
60 vvcsvalfyfraqmdpnrisedgthciylrilrhenadfgdtlesqdtklipdscri 119

QY 119 KQAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAASIPSGS 178
120 kqafgavqkelqhvgsqhiraekamvsgswldakrskleaqpfahltinatdipsgs 179

QY 179 HKVTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYLANICFRHHETSGVPTDYQLQM 238
180 hkvsisswyhdcrgwakisnmtfsgngklivnqdgfylylanicfrhhetsgdlateyqlm 239

QY 239 VYVKTSTIKIPSSHNLKMGSTKNWSEFHFYSINVGFFKLRAGEEISIQVSNPSLL 298
240 vyvktstikipsstlmkgsstkynwsefhfysinvvgffklrgeeisievsnpsll 299

QY 299 DPDQDATYFGAFKVDID 316
300 dpdqdatyfgafkvridd 317

RESULT 15
AAW69957
ID AAW69957 standard; Protein; 317 AA.
XX
AC AAW69957;
XX
DT 08-OCT-1998 (first entry)
XX
NF-kB receptor activator RANK ligand (RANKL).
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
OS Homo sapiens.
XX
PN W09828426-A2.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-US23775.
XX
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
PA (IMMUNEX) IMMUNEX CORP.
XX
PI Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR WPI: 1998-377657/32.
DR N-PSDB: AAV41378.
XX

PT New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
PS Claim 27; Pages 59-60; 80pp; English.
XX
CC This represents a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.
XX
SQ Sequence 317 AA;

Query Match 84.6%; Score 1417.5; DB 19; Length 317;
Best Local Similarity 84.3%; Pred. No. 4.4e-120;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYLRSEEMSGPGVHEGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 mrrasrdytkylrgseemggpgaphegplh-appppahqpapaarsmfvallglgq 59

QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLDSTLESDT--LPDSCRMM 118
60 vvcsvalfyfraqmdpnrisedgthciylrilrhenadfgdtlesqdtklipdscri 119

QY 119 KQAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQRKPEAQPFALHTINAASIPSGS 178
120 kqafgavqkelqhvgsqhiraekamvsgswldakrskleaqpfahltinatdipsgs 179

QY 179 HKVTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYLANICFRHHETSGVPTDYQLQM 238
180 hkvsisswyhdcrgwakisnmtfsgngklivnqdgfylylanicfrhhetsgdlateyqlm 239

QY 239 VYVKTSTIKIPSSHNLKMGSTKNWSEFHFYSINVGFFKLRAGEEISIQVSNPSLL 298
240 vyvktstikipsstlmkgsstkynwsefhfysinvvgffklrgeeisievsnpsll 299

QY 299 DPDQDATYFGAFKVDID 316
300 dpdqdatyfgafkvridd 317

Search completed: July 15, 2002, 11:02:28
Job time: 83 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 11:01:30 ; Search time 30.24 Seconds
(without alignments)
1807.751 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSEMG.....LLDPQDQATYGFQVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 173994929 residues 562222
All number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1646.5	98.3	313	11	Q9RLY0	Q9RLY0 mus musculu
2	1597	95.3	318	11	Q9ESE2	Q9ESE2 rattus norv
3	1476.5	88.1	287	11	Q9JJK9	Q9JJK9 mus musculu
4	1220	72.8	270	4	Q9GQ17	Q9GQ17 homo sapien
5	1057	63.1	199	11	Q9JJK8	Q9JJK8 mus musculu
6	272	16.2	53	11	Q9LZ19	Q9LZ19 rattus norv
7	263.5	15.7	214	13	Q9DDZ5	Q9DDZ5 brachydanio
8	217.5	13.0	287	13	Q9OWT9	Q9OWT9 gallus gall
9	188.5	11.3	261	6	Q9BDN3	Q9BDN3 callithrix
10	182.5	10.9	261	6	Q9BDM3	Q9BDM3 aotus trivi
11	179.5	10.7	282	6	Q9BEA8	Q9BEA8 sus scrofa
12	179.5	10.7	282	6	Q9SM04	Q9SM04 sus scrofa
13	179	10.7	280	6	Q9BDM5	Q9BDM5 macaca mula
14	178.5	10.7	282	6	Q9BN10	Q9BN10 sus scrofa
15	178	10.6	280	6	Q9MYL6	Q9MYL6 macaca neme
16	177	10.6	280	6	Q9BDN1	Q9BDN1 cercocebus

17	176.5	10.5	261	6	Q9BDC7	Q9BDC7 macaca mula
18	168.5	10.1	272	13	Q918D8	Q918D8 gallus gall
19	151	9.0	240	6	Q9BDM7	Q9BDM7 macaca neme
20	149	8.9	234	6	Q9TTJ3	Q9TTJ3 equus cabal
21	148	8.8	232	11	Q35853	Q35853 mus musculu
22	147.5	8.8	310	11	Q9JWL0	Q9JWL0 marmota mon
23	146.5	8.7	239	11	Q9QYH9	Q9QYH9 mus musculu
24	145	8.7	260	11	Q9Z2V2	Q9Z2V2 rattus norv
25	145	8.7	260	11	Q9R254	Q9R254 rattus norv
26	142	8.5	232	4	Q9UIV3	Q9UIV3 homo sapien
27	140.5	8.4	310	11	Q9JWL1	Q9JWL1 marmota mon
28	140	8.4	174	4	Q95150	Q95150 homo sapien
29	139	8.3	234	6	Q28320	Q28320 capra hircu
30	136	8.1	191	6	Q9MYZ2	Q9MYZ2 tamiasciuru
31	133.5	8.0	215	11	Q99ND1	Q99ND1 tamiasciuru
32	133	7.9	157	4	O43647	O43647 homo sapien
33	132	7.9	149	6	O97543	O97543 aotus nancy
34	132	7.9	217	11	Q9ERG6	Q9ERG6 peromyscus
35	131.5	7.9	156	11	Q91ZL4	Q91ZL4 sigmodon hi
36	131	7.8	149	6	O97538	O97538 aotus vocif
37	131	7.8	149	6	O9TTG8	O9TTG8 aotus nigri
38	130	7.8	204	4	O96LD2	O96LD2 homo sapien
39	130	7.8	216	11	O70332	O70332 mesocricetu
40	128.5	7.7	233	6	Q9BEAL	Q9BEAL tursiops tr
41	127.5	7.6	217	6	Q9BEC5	Q9BEC5 tenrec ecau
42	126.5	7.6	217	6	Q9BEG1	Q9BEG1 bradypus tr
43	126.5	7.6	217	6	Q9BEG0	Q9BEG0 cyclopes di
44	126.5	7.6	250	6	Q9XTA7	Q9XTA7 macropus eu
45	126	7.5	216	6	Q9BEC9	Q9BEC9 ochotona pr

ALIGNMENTS

RESULT 1

Q9RLY0	Q9RLY0	PRELIMINARY;	PRT;	313 AA.
AC	Q9RLY0;			
DT	01-MAY-2000 (TReMBLrel. 13, Created)			
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TReMBLrel. 13, Last annotation update)			
DE	OSTEOCLAST DIFFERENTIATION FACTOR.			
GN	TNFSF11.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129;			
RX	MEDLINE=99214075; PubMed=10196481;			
RA	Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,			
RA	Ueda M., Higashio K.;			
RT	"Cloning and characterization of the gene encoding mouse osteoclast			
RT	differentiation factor."			
RL	Gene 230.121-127(1999).			
DR	EMBL; AB022039; BAA36970.1;			
DR	EMBL; AB022036; BAA36970.1; JOINED.			
DR	EMBL; AB022037; BAA36970.1; JOINED.			
DR	HSSP; P50591; 1D0G.			
DR	MGD; MGI:1100089; Tnfsf11.			
DR	InterPro; IPR003263; TNF_5.			
DR	InterPro; IPR00478; TNF_family.			
DR	Pfam; PF00229; TNF; 1.			
DR	ProDom; PD008600; TNF_5; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00049; TNF.2; 1.			
SQ	SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;			

Query Match 98.3%; Score 1646.5; DB 11; Length 313;
Best Local Similarity 99.1%; Pred. No. 4.3e-139;

```
Matches 313; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 MRRASRDYGYKYLRSSEEMSGSGVPEHGLHPAPAPAPAPPAASRSRMFLALLGLGLGQ 60
DB 1 MRRASRDYGYKYLRSSEEMSGSGVPEHGLHPAPAPAPAPPAASRSRMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMQ 120
DB 61 VVCSIALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMQ 120
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAQPPFAHLTINAAIPSGSHK 180
DB 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAQPPFAHLTINAAIPSGSHK 177
QY 181 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQMY 240
DB 178 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQMY 237
QY 241 VVKTSIKIPSSHNLKMGSTKNWNSGSEFHFYSINVGFFKLRAGEEISIOVSNPSLLDP 300
DB 238 VVKTSIKIPSSHNLKMGSTKNWNSGSEFHFYSINVGFFKLRAGEEISIOVSNPSLLDP 297
QY 301 DQDATYFGAFKVDQID 316
DB 298 DQDATYFGAFKVDQID 313
RESULT 2
Q9ESE2 PRELIMINARY; PRT; 318 AA.
AC Q9ESE2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RL J. Bone Miner. Res. 15:2178-2186(2000).
DR EMBL: AF187319; AAC17031.1; -.
DR HSSP: P50591; 100G.
DR InterPro: IPR003263; TNF_5.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;
Query Match 95.3%; Score 1597; DB 11; Length 318;
Best Local Similarity 95.0%; Pred. No. 1.2e-134;
Matches 302; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
QY 1 MRRASRDYGYKYLRSSEEMSGSGVPEHGLHPAPAPAPPAASRSRMFLALLGLGLGQ 60
DB 1 MRRASRDYGYKYLRSSEEMSGSGVPEHGLHPAPAPAPPAASRSRMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRM 118
DB 61 VVCSIALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRM 120
QY 119 KOAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAQPPFAHLTINAAIPSGS 178
DB 121 KOAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAQPPFAHLTINAAIPSGS 180
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QY 179 HKVTLSSWYHDSRWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQ 238
DB 181 HKVTLSSWYHDSRWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQ 240
QY 239 VVVKTSIKIPSSHNLKMGSTKNWNSGSEFHFYSINVGFFKLRAGEEISIOVSNPSLL 298
DB 241 VVVKTSIKIPSSHNLKMGSTKNWNSGSEFHFYSINVGFFKLRAGEEISIOVSNPSLL 300
QY 299 DPQDATYFGAFKVDQID 316
DB 301 DPQDATYFGAFKVDQID 318
RESULT 3
Q9JJK9 PRELIMINARY; PRT; 287 AA.
AC Q9JJK9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 2.
GN TNFSF11 OR RANKL 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21150053; PubMed=11250921;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT "Determination of Three Isoforms of the Receptor Activator of Nuclear
RT Factor-kappaB Ligand and Their Differential Expression in Bone and
RT Thymus."
RL Endocrinology 142:1419-1426(2001).
DR EMBL: AB032771; BAA97257.1; -.
DR HSSP: P50591; 1D0G.
DR MGD: MGI:1100089; Tnfsf11.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32234 MW; 8B2CE8B4C7B534CC CRC64;
Query Match 88.1%; Score 1476.5; DB 11; Length 287;
Best Local Similarity 90.2%; Pred. No. 6e-124;
Matches 285; Conservative 1; Mismatches 1; Indels 29; Gaps 1;
QY 1 MRRASRDYGYKYLRSSEEMSGSGVPEHGLHPAPAPAPPAASRSRMFLALLGLGLGQ 60
DB 1 MRRASRDYGYKYLRSSEEMSGSGVPEHGLHPAPAPAPPAASRSRMFLALLGLGLGQ 31
QY 61 VVCSIALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMQ 120
DB 32 VVCSIALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMQ 91
QY 121 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAQPPFAHLTINAAIPSGSHK 180
DB 92 AFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQRGKPEAQPPFAHLTINAAIPSGSHK 151
QY 181 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQMY 240
DB 152 VTLSSWYHDSRWAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLQMY 211
QY 241 VVKTSIKIPSSHNLKMGSTKNWNSGSEFHFYSINVGFFKLRAGEEISIOVSNPSLLDP 300
DB 212 VVKTSIKIPSSHNLKMGSTKNWNSGSEFHFYSINVGFFKLRAGEEISIOVSNPSLLDP 271
```



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DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TRAIL-LIKE PROTEIN.
GN TNFSF10L.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR EMBL; AF250041; AAG47640.1; -.
DR HSSP; P50591; 1D0G.
DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD02012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 15.7%; Score 263.5; DB 13; Length 214;
Best Local Similarity 31.5%; Pred. No. 1.le-15;
Matches 69; Conservative 42; Mismatches 77; Indels 31; Gaps 6;

QY 117 MKQAFQAVQKELQHVGPQFSGAPAMME-----GS--WLDVAQKGPQAPFAHLTI 169
DB 2 KLAEGIKAVISKVDSIIISKQLHAARTQTHSYNTGSKFMTVMQR-----PSAHLTL 55

QY 170 NAASIPS-----GSHKVTLSWSYHDSRGWAKISNMNLTSLNGKLRVNDQGFYYL 215
DB 56 SSASDNSRPSQSDHQPOFDLQSCRPVHTWANKSGAHLNMTLTNGRLRVPDQGRYYL 115

QY 216 YANICFRHHETSGVPTDYQLQMLVYV--KTSIKIPSSHNLMKGGSTKWSGNSSEHFYS 273
DB 116 VQVYFRYPSDSDQSSVSHQLVQCIYKTSYLNPI--QLLKGVGTKCWAPDAEYALHS 173

QY 274 INVGGFFKLAGEEISIOVSNPSLDPDQDATYFGAFKV 312
DB 174 VYQGLFELRAGDEVFVSVSPTWYGEDSSSYFGAFRL 212

RESULT 8
Q90WT9 PRELIMINARY; PRT; 287 AA.
AC Q90WT9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE TNF-RELATED APOPTOSIS INDUCING LIGAND.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Brigham J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY07941; AAL23702.1; -.
SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;
```

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Query Match 13.0%; Score 217.5; DB 13; Length 287;
Best Local Similarity 26.7%; Pred. No. 2.le-11;
Matches 66; Conservative 51; Mismatches 103; Indels 27; Gaps 8;

QY 81 SEDSTHCFFYILRLHENAGLDQSTLESEDYLPDSCRRMKQAFQGVQKELQHVGPQRF 140
DB 51 SSELRCLQLINQOEGSNLEE--LISN-----QSCLKANTIKAYATVTVENVISRSV 104
QY 141 GAPAMMEGSLDVAQ---RGKPEAQPFALHTI---NAASIPSG-----SHKVTLSW 186
DB 105 EA---QKSYFNISEGOVATKTLGKPSAHLIFRPNPAQDGSSRRFGLNSQSCRHAITRW 160
QY 187 YHDSGWAKISNMNLTSLNGKLRVNDQGFYYLYANICFRHHETSGVPTDYQLQMLVYV-VKTS 245
DB 161 EDSTIHSHLQNTYRDGRLRVNAGKYVYSQIYFRYSRDGAGARVSPVQLVQVINNKT 220
QY 246 IKIPSSHNLMKGGSTKWSGNSSEHFYSINVGGFFKLAGEEISIOVSNPSLDPDQDAT 305
DB 221 YSQPIL--LLKGVGTCWAPAEAYGLHALYQGLFELKAGDELFLVSVSLAIDYSDAAS 278
QY 306 YFGAFKV 312
DB 279 YFGAFRL 285

RESULT 9
Q9BDN3 PRELIMINARY; PRT; 261 AA.
AC Q9BDN3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DIC-2001 (TREMBLrel. 19, Last annotation update)
DE CD154 PROTEIN.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344844; AAK37603.1; -.
DR HSSP; P29965; 1ALY.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 261 AA; 29360 MW; 10CA588D923754EB CRC64;

Query Match 11.3%; Score 188.5; DB 6; Length 261;
Best Local Similarity 25.8%; Pred. No. 7.3e-09;
Matches 77; Conservative 49; Mismatches 110; Indels 63; Gaps 16;

QY 32 PAPSAPAPAPPAASRSKMFALLGLGVQVVCSTALF-LYFRAQMDPNRSTEDSTHCFYR 90
DB 8 PVPRSAATGPP--VSMKIFWLLTVLITQIGSALFAYLHRLD--KTEDR----- 57
QY 91 ILRLHE-----NAGLDQSTLESEDYLPDSCRRMKQAFQGVQKELQHVGPQRF 139
DB 58 --NLHDEDFVEMKTIQRCNTGERSLSLL-----NCEIKSQFEGFV-KDIM-----L 100
QY 140 SGAPAMMEGSLDVAQKGPQAPFAHLTNAASIPSGSHKVTLSWSYHDSRGWAKISN-- 197
DB 101 NKEKKKENSF--EMQKGDQNPQIAAHV-----ISEASSKTTSLQWAEKGYTMSNNL 152
```

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	185.5	11.1	261	2	S53090	CD40 ligand - bovi
2	183	10.9	278	2	A5266	fas ligand - rat
3	182	10.9	279	2	A53062	Fas ligand - mouse
4	173.5	10.4	281	2	I38707	Fas ligand - human
5	171.5	10.2	261	2	I53476	CD40 ligand - huma
6	157	9.4	260	2	S21738	CD40 ligand - mous
7	149	8.9	234	1	J01344	tumor necrosis fac
8	146.5	8.7	235	1	QWNSN	tumor necrosis fac
9	143.5	8.6	233	1	S22052	tumor necrosis fac
10	141	8.4	234	1	JH0529	tumor necrosis fac
11	140	8.4	233	2	S11688	tumor necrosis fac
12	139.5	8.3	233	1	QWUN	tumor necrosis fac
13	137.5	8.2	234	1	A25451	tumor necrosis fac
14	135.5	8.1	235	2	I54490	tumor necrosis fac
15	133.5	8.0	233	1	S24642	tumor necrosis fac
16	133	7.9	185	2	S52715	tumor necrosis fac
17	133	7.9	232	1	S12606	tumor necrosis fac
18	129.5	7.7	235	2	JU0029	tumor necrosis fac
19	129.5	7.7	306	2	I49139	lymphotoxin-beta -
20	117	7.0	244	2	A46066	lymphotoxin beta -
21	115.5	6.9	193	2	S06192	tumor necrosis fac
22	103.5	6.2	340	2	S49742	hypothetical prote
23	103	6.1	3848	2	T17414	tipc protein - sli
24	99.5	5.9	558	2	T23649	hypothetical prote
25	99	5.9	440	2	I49681	glyceraldehyde-3-p
26	97	5.8	450	2	S8114	hypothetical prote
27	95.5	5.7	553	2	S55514	dihydrolipoamide S
28	94	5.6	1486	1	B40333	collagen alpha 1(I
29	93.5	5.6	205	1	QWUX3	lymphotoxin alpha

Cell 75, 1169-1178, 1993

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 11:01:55 ; Search time 13.43 Seconds
(without alignments)
911.048 Million cell updates/sec

Title: US-09-671-658A-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSEEMG.....LLDPDQATYFGAFKVDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
1 number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1675	100.0	316	1	TN11_MOUSE
2	1417.5	84.6	317	1	TN11_HUMAN
3	258.5	15.4	281	1	TN10_HUMAN
4	244	14.6	291	1	TN10_MOUSE
5	185.5	11.1	261	1	TNF5_BOVIN
6	183	10.9	278	1	FASL_RAT
7	182	10.9	279	1	FASL_MOUSE
8	173.5	10.4	281	1	FASL_HUMAN
9	171.5	10.2	261	1	TNF5_HUMAN
10	164	9.8	260	1	TNF5_FELCA
11	157	9.4	234	1	TNFA_CAVPO
12	157	9.4	260	1	TNF5_MOUSE
13	154	9.2	260	1	TNF5_CANFA
14	149	8.9	234	1	TNFA_HORSE
15	148.5	8.9	233	1	TNFA_MACFA
16	147.5	8.8	233	1	TNFA_MACMU
17	146.5	8.7	235	1	TNFA_MOUSE
18	143.5	8.6	233	1	TNFA_PAPHU
19	143.5	8.6	233	1	TNFA_PAPSP
20	141	8.4	234	1	TNFA_SHEEP
21	140	8.4	233	1	TNFA_FELCA
22	139.5	8.3	233	1	TNFA_CANFA
23	139.5	8.3	233	1	TNFA_HUMAN
24	137	8.2	235	1	TNFA_RABIT
25	135.5	8.1	235	1	TNFA_PERLE
26	134.5	8.0	240	1	TN14_HUMAN
27	133.5	8.0	233	1	TNFA_BOVIN
28	133	7.9	232	1	TNFA_PIG
29	129.5	7.7	233	1	TNFA_MARMO
30	129.5	7.7	235	1	TNFA_RAT
31	129.5	7.7	306	1	TNFC_MOUSE
32	128	7.6	229	1	TNFA_CEREL
33	117	7.0	244	1	TNFC_HUMAN

34	115.5	6.9	193	1	TNFA_CAPHI
35	109.5	6.5	233	1	TNFA_MACEU
36	109	6.5	201	1	TNFB_MACEU
37	103.5	6.2	340	1	YMD7_YEAST
38	99	5.9	440	1	G3PT_MOUSE
39	97	5.8	450	1	YK22_YEAST
40	95.5	5.7	553	1	ODP2_ALCEU
41	93.5	5.6	205	1	TNFB_HUMAN
42	92.5	5.5	197	1	TNFB_RABIT
43	91	5.4	616	1	SPAS_HUMAN
44	90.5	5.4	658	1	PAK1_SCHPO
45	89	5.3	1694	1	SN_MOUSE

RESULT 1
TN11_MOUSE
ID TN11_MOUSE STANDARD; PRT; 316 AA.
AC O35235; O35306;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor) (OCIF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;
RA "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."; J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;
RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; Cell 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow stroma;
RX MEDLINE=98188248; PubMed=9520411;
RA Yasuda H., Shima N., Nakagawa N., Yanaguchi K., Kinoshita M., Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RA "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL."; Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymic lymphoma;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,

ALIGNMENTS


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DR PDB: 1D0G; 22-OCT-99.
DR PDB: 1D4V; 01-NOV-99.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR Cytokine; Transmembrane; Signal-anchor; Apoptosis; 3D-structure.
KW CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 3.3e-14;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAARSMLALLGLGLGVGVCSIALFYLFRAQMD--PNRISDSTHCFYRLRLHENAGL 100
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDQKYSKGIACF-----LKEDDSY 64

QY 101 QDSTLESDTLFDCRRMKQAFQGAQVK-----ELQHVGPQRPFSGAPAMM 146
DB 65 WDP--NDESNMSPCQVQWQLRVKMLRTSEETISTVQEKQONISPL----- 113

QY 147 EGSWLDVAQRGKPEAQPFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 114 -----VREGRQVAV-----AHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165

QY 197 NMTLSNGKLRVNDGFFYLYLANICFRHETSGSVPTDYLQLMVYVYVTKTSIKIPSSHNLKM 256
DB 166 NLHRLNGELVTHNGFYLYISQTYFRFQEAEDASKMVKDKVTKQLVQYIKYT-STPDPILLMK 224

QY 257 GGSTKNWNSGSEFHYISVNGGFFKLAGEEISIOVSNPSLLDPDQDATYFGAFKV 312
DB 225 SARNSCWSKDAEYGLYSIQGIFELKENDRIFVSVTNEHLMDMBDEASFFGAFLV 280

RESULT 4
TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein).
GN TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis.";
RL Immunity 3:673-682(1995).
CC -1- FUNCTION: INDUCES APOPTOSIS.
CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U37522; AAC52345.1; -.
CC MGD; MGI:107414; Tnfsf10.
CC InterPro: IPR003263; TNF_5.
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF; 1.
CC ProDom: PD002012; TNF_abc; 1.
CC ProDom: PD008600; TNF_5; 1.
CC SMART: SM00207; TNF; 1.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS00049; TNF_2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Apoptosis.
KW CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.6%; Score 244; DB 1; Length 291;
Best Local Similarity 27.5%; Pred. No. 5.3e-13;
Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

QY 52 ALLGLGLGQ-----VVCSTAL-----FLVFRQMD--PNRISDSTHCFYRIL 92
DB 6 ALKDLFSQHFRRMMVICVLLQVLLQAVSVAVTYFTNEMKQLQDNYSKIGLACFSK-- 63

QY 93 RUHENAGLQDSTLESDTLFDCSC-----RRMKQAFQGAQVQKELQHVIG--PQFSGAPAMM 146
DB 64 ----TDEFWDST--DGEILNRPCLOVKKQYQLIEVTLRTFQDTISTVPEKQLSTPPLP 118

QY 147 EGSWLDVAQRGKPEAQPFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 119 RG-----GRPQ-KVAHITGTRNSALIPISKDGTGLQKIESWESSRKGHSFLN 169

QY 197 NMTLSNGKLRVNDGFFYLYLANICFRHETSGSVPTDYLQLMVYVYVTKTSIKIPS 250
DB 170 HVLFRNGELVIEQGLYIYSQTYFRFQEAEDASKMVKDKVTKQLVQYIKYT-SYPD 228

QY 251 SHNLKMGSGSTKNWNSGSEFHYISVNGGFFKLAGEEISIOVSNPSLLDPDQDATYFGAF 310
DB 229 PIVLMKSARNSCWSRDAEYGLYSIQGIFELKKNDRIFVSVTNEHLMDLQDEASFFGAF 288

QY 311 KV 312
DB 289 LI 290

RESULT 5
TNF5_BOVIN STANDARD; PRT; 261 AA.
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen
DE GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;

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